

SEQUENCE LISTING

<110> SunGene GmbH & Co.KGaA

<120> Transgenic expression cassettes for expressing nucleic acids
in the flower of plants

<130> AE20020666

<140>

<141>

<160> 83

<170> PatentIn Ver. 2.1

<210> 1

<211> 312

<212> DNA

<213> Tagetes erecta

<220>

<221> promoter

<222> (1)..(312)

<400> 1

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aattaaaata aagagaagag aaagattaag aggggtgatgg ggatattaaa gacggscaat 180
atagtgatgc cacgtagaaa aaggtaagtg aaaacatata acgtggcttt aaaagatggc 240
ttggctgcta atcaactcaa ctcaactcat atcctatcca ttcaaattca attcaattct 300
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<210> 2

<211> 447

<212> DNA

<213> Tagetes erecta

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<221> promoter

<222> (1)..(312)

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<222> (313)..(444)

<220>

<221> misc_feature

<222> (445)..(447)

<223> ATG-start codon

<400> 2

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aattaaaata aagagaagag aaagattaag aggggtgatgg ggatattaaa gacggscaat 180
atagtgatgc cacgtagaaa aaggtaagtg aaaacatata acgtggcttt aaaagatggc 240
ttggctgcta atcaactcaa ctcaactcat atcctatcca ttcaaattca attcaattct 300
attgaatgca aagcaaagca aaggttggtt gttgttggtt ttgagagaca ctccaatcca 360
aacagatata aggcgtgact ggatatttct ctctcgttcc taacaacagc aacgaagaag 420
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<210> 3

<211> 537

<212> DNA

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<221> promoter

<222> (1)..(312)

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<222> (313)..(444)

<220>

<221> sig_peptide

<222> (445)..(537)

<220>

<221> CDS

<222> (445)..(537)

<223> coding for transit peptide of epsilon cyclase

<400> 3

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 aattaaata aagagaagag aaagattaag aggggtgatgg ggatattaaa gacggscaat 180
 atagtgatgc cacgtagaaa aaggtaagtg aaacatata acgtggcttt aaaagatggc 240
 ttggctgcta atcaactcaa ctcaactcat atcctatcca ttcaaattca attcaattct 300
 attgaatgca aagcaaagca aaggttgttt gttgtgtgtg ttgagagaca ctccaatcca 360
 aacagataca aggcgtgact ggatatttct ctctcgttcc taacaacagc aacgaagaag 420
 aaaaagaatc attactaaca atca atg agt atg aga gct gga cac atg acg 471

Met Ser Met Arg Ala Gly His Met Thr

1

5

gca aca atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga 519
 Ala Thr Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg
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tac acg aag caa att aag 537
 Tyr Thr Lys Gln Ile Lys
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<212> PRT

<213> Tagetes erecta

<400> 4

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Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys
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<210> 5

<211> 456

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(6)

<223> restriction site

<220>

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<222> (451)..(456)

<223> restriction site

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 <221> misc_feature
 <222> (7)..(450)
 <223> coding for promoter and 5'-UTR region

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 ttaattaaaa taaagagaag agaaagatta agaggggtgat ggggatatta aagacggsca 180
 atatagtgat gccacgtaga aaaaggtaag tgaaaacata caacgtggct ttaaaagatg 240
 gcttggctgc taatcaactc aactcaactc atatcctatc cattcaaatt caattcaatt 300
 ctattgaatg caaagcaaag caaagggttg ttgttgttgg ttgttgagaga cactccaatc 360
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 agaaaaagaa tcattactaa caatcaatgg ccatgg 456

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 <213> *Tagetes erecta*

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 <222> (1)..(6)
 <223> restriction site

<220>
 <221> misc_feature
 <222> (538)..(543)
 <223> restriction site

<220>
 <221> misc_feature
 <222> (7)..(542)
 <223> coding for promoter - 5'-UTR - signal peptide
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 ttaattaaaa taaagagaag agaaagatta agaggggtgat ggggatatta aagacggsca 180
 atatagtgat gccacgtaga aaaaggtaag tgaaaacata caacgtggct ttaaaagatg 240
 gcttggctgc taatcaactc aactcaactc atatcctatc cattcaaatt caattcaatt 300
 ctattgaatg caaagcaaag caaagggttg ttgttgttgg ttgttgagaga cactccaatc 360
 caaacagata caaggcgtga ctggatattt ctctctcgtt cctaacaaca gcaacgaaga 420
 agaaaaagaa tcattactaa caatcaatga gtatgagagc tggacacatg acggcaacaa 480
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 tgg 543

<210> 7
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 <213> *Arabidopsis thaliana*

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 gctgcgtatt ctactacaa tgtggccaca cagacctcgt ttcttcagct gatgaatgat 180
 ggcgctaattg tctcaaagca aaagggtttc gatgtgttca acgcgttgga tgtgatgcac 240
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 ctctacaatt accgtttgaa aagtgccttg aagccagcgg aactcgggct tgttctctta 360
 taagctcaac aacttgattt gatggtatca acaaacttga aatttgtctc tctttttttt 420
 tcttcagtct gaactacttc tcccatggtt tactgaaact gagtttaatt attttggcaa 480

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tgcaattttg gatttttgctt ttagtttcac ttgtgttctc tgagagagtt gaccctgaga 540
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tagctacggc ccatctatcg tagaagttgt tttttgtact aaagcctgtt atagccgaac 660
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aaaggaaata attagattcc tctttctgct tgctatacct tgatagaaca atataacaat 960
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<210> 8

<211> 1169

<212> DNA

<213> *Oryza sativa*

<400> 8

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gggaagcagc ggacgatgcc gagcaggaca atgtcctcct cgtcaccacc ttcctcatcg 180
tcgtcgcggt cgggtgggtgc cgggcggagc gggtttttgag ggaggggtcg gcggccggcg 240
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ggacgacgac gaggaaggag ggagagagga atcaactacc gacgacagcg gaggcgggcg 360
agcgcggtgc cgggctgctc acgctcgccg accaggccct cgctccgtca cactcgctcg 420
cctccgttcc acccgagccc cgcgcgcgtc cgttcgagc gctcgccgt cgccgctccg 480
ctgctgtgca gtcccgcgcg cgcgctcgcc ctgactgaag aagaaaagag agaagagaga 540
aaagagaagg gaaggagaag aaaatagaag aaaaaaatat gtgcagctga tgtatgagcc 600
ccacatactc ttttttaatc ttttttgctg actacgatgc cagtcagcg aaaccaccta 660
tatatactac cataggatct tgagtgcacg gtttatatga gtttaggagt atacattttt 720
agttttatgg ttaagggatc ataaaaaatt ctcgctatta agttgagtga cgcgcagtga 780
acttattact caaacttaac agcgtttgat ccattcacat ccggcccata gcagcccata 840
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accgctccc tctcctctc cctcctccta caatggccgc agcagcagca gccagcagca 1080
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<210> 9

<211> 1830

<212> DNA

<213> *Tagetes erecta*

<220>

<221> CDS

<222> (141)..(1688)

<223> coding for epsilon-cyclase

<400> 9

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agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173
Met Ser Met Arg Ala Gly His Met Thr Ala Thr
1 5 10
atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221
Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr
15 20 25
aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa 269
Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln
30 35 40

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gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tgc gag ctg	317
Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu	
45 50 55	
ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc	365
Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser	
60 65 70 75	
cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt	413
Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser	
80 85 90	
aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt	461
Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu	
95 100 105	
gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc	509
Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile	
110 115 120	
ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa	557
Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu	
125 130 135	
ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat	605
Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp	
140 145 150 155	
act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc	653
Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala	
160 165 170	
tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg	701
Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg	
175 180 185	
tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att	749
Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile	
190 195 200	
act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc	797
Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile	
205 210 215	
aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga	845
Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly	
220 225 230 235	
aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca	893
Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr	
240 245 250	
gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc	941
Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	
255 260 265	
cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989
Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	
270 275 280	
tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037
Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	
285 290 295	
cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc	1085
Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	
300 305 310 315	

atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act 1133
 Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr
 320 325 330

atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att 1181
 Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile
 335 340 345

cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt 1229
 Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe
 350 355 360

ggt gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta 1277
 Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val
 365 370 375

aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att 1325
 Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile
 380 385 390 395

tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca 1373
 Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr
 400 405 410

acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg 1421
 Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg
 415 420 425

aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag 1469
 Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln
 430 435 440

atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg 1517
 Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu
 445 450 455

ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act 1565
 Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr
 460 465 470 475

gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc 1613
 Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser
 480 485 490

ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga 1661
 Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly
 495 500 505

aca atg tta aaa gcg tat ctc acg ata taaataactc tagtcgcgat 1708
 Thr Met Leu Lys Ala Tyr Leu Thr Ile
 510 515

cagtttagat tataggcaca tcttgcatat atatattgtat aaaccttatg tgtgctgtat 1768
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 gg 1830

<210> 10
 <211> 516
 <212> PRT
 <213> Tagetes erecta
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 Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
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		35					40					45					
Glu	Asp	Tyr	Val	Lys	Ala	Gly	Gly	Ser	Glu	Leu	Leu	Phe	Val	Gln	Met		
	50					55					60						
Gln	Gln	Asn	Lys	Ser	Met	Asp	Ala	Gln	Ser	Ser	Leu	Ser	Gln	Lys	Leu		
65					70					75					80		
Pro	Arg	Val	Pro	Ile	Gly	Gly	Gly	Gly	Asp	Ser	Asn	Cys	Ile	Leu	Asp		
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Leu	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Gly	Glu		
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Ser	Ala	Lys	Leu	Gly	Leu	Asn	Val	Ala	Leu	Ile	Gly	Pro	Asp	Leu	Pro		
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Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Ile	Gly	Leu	Gly		
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Arg	Asp	Leu	Leu	His	Glu	Glu	Leu	Leu	Thr	Arg	Cys	Met	Glu	Ser	Gly		
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Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala	Pro	Asn		
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Gly	Leu	Ser	Leu	Ile	Glu	Cys	Glu	Gly	Asn	Ile	Thr	Ile	Pro	Cys	Arg		
	210					215					220						
Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Gln	Tyr		
225					230					235					240		
Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Ile	Glu		
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Val	Glu	Val	Glu	Ser	Ile	Pro	Tyr	Asp	Pro	Ser	Leu	Met	Val	Phe	Met		
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Asp	Tyr	Arg	Asp	Tyr	Thr	Lys	His	Lys	Ser	Gln	Ser	Leu	Glu	Ala	Gln		
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Tyr	Pro	Thr	Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	Pro	Thr	Lys	Val	Phe		
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305					310					315					320		
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Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu		
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Ala	Pro	Asn	Tyr	Ala	Ala	Val	Ile	Ala	Lys	Ile	Leu	Gly	Lys	Gly	Asn		
385					390					395					400		
Ser	Lys	Gln	Met	Leu	Asp	His	Gly	Arg	Tyr	Thr	Thr	Asn	Ile	Ser	Lys		
				405					410					415			

Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
 420 425 430
 Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445
 Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460
 Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480
 Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
 485 490 495
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 500 505 510
 Tyr Leu Thr Ile
 515

<210> 11
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 <212> DNA
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<220>
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 tcgttcctta acaacagcaa cgaagaagaa aaagaatcat tactcacaat ca atg agt 178
 Met Ser
 1
 atg aga gct gga cac atg acg gca aca atg gcg gct ttt aca tgc cct 226
 Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr Cys Pro
 5 10 15
 agg ttt atg act agc atc aga tac acg aag caa att aag tgc aac gct 274
 Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys Asn Ala
 20 25 30
 gct aaa agc cag cta gtc gtt aaa caa gag att gag gag gaa gaa gat 322
 Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu Glu Asp
 35 40 45 50
 tat gtg aaa gcc ggt gga tcg gag ctg ctt ttt gtt caa atg caa cag 370
 Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met Gln Gln
 55 60 65
 aat aag tcc atg gat gca cag tct agc cta tcc caa aag ctc cca agg 418
 Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu Pro Arg
 70 75 80
 gta cca ata gga gga gga gga gac agt aac tgt ata ctg gat ttg gtt 466
 Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp Leu Val
 85 90 95
 gta att ggt tgt ggt cct gct ggc ctt gct ctt gct gga gaa tca gcc 514
 Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu Ser Ala
 100 105 110

aag cta ggc ttg aat gtc gca ctt atc ggc cct gat ctt cct ttt aca	562
Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro Phe Thr	
115 120 125 130	
aat aac tat ggt gtt tgg gag gat gaa ttt ata ggt ctt gga ctt gag	610
Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly Leu Glu	
135 140 145	
ggc tgt att gaa cat gtt tgg cga gat act gta gta tat ctt gat gac	658
Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu Asp Asp	
150 155 160	
aac gat ccc att ctc ata ggt cgt gcc tat gga cga gtt agt cgt gat	706
Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Asp	
165 170 175	
tta ctt cac gag gag ttg ttg act agg tgc atg gag tca ggc gtt tca	754
Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly Val Ser	
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Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr	
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Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln Tyr Pro	
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Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu Leu Lys	
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Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile Thr Lys	
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Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu	
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Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser	
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 Arg Leu Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser
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 Ser Thr Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro
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 His Ser Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr
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 Gly Gly Thr Met Leu Lys Ala Tyr Leu Thr Ile
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Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr Phe Pro Ser Trp																
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Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr Ser Tyr Arg Asn																
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Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly Gly Gly Ser Ser																
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Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe Ala Asp Glu Glu																
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Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val Asp Lys Leu Pro																
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Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp Leu Val Val Ile Gly Cys																
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Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu																
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Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly																
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Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln Lys Cys Ile Glu																
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His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp Asp Lys Pro Ile																
165 170 175 180																

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Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg Leu Leu His Glu	
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Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser	
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Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu Arg Leu Val Ala	
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Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala Thr Val Ala Ser	
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Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro Pro Glu Arg Lys	
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14

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 Met Ile Lys Thr Tyr Leu Lys Val
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 Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
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 Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
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 Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
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15

Tyr	Leu	Ser	Ser	Lys	Val	Asp	Ser	Ile	Thr	Glu	Ala	Ser	Asp	Gly	Leu	210	215	220
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Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	260	265	270
Val	Glu	Asn	Ser	Pro	Tyr	Asp	Pro	Asp	Gln	Met	Val	Phe	Met	Asp	Tyr	275	280	285
Arg	Asp	Tyr	Thr	Asn	Glu	Lys	Val	Arg	Ser	Leu	Glu	Ala	Glu	Tyr	Pro	290	295	300
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Glu	Thr	Cys	Leu	Ala	Ser	Lys	Asp	Val	Met	Pro	Phe	Asp	Leu	Leu	Lys	325	330	335
Thr	Lys	Leu	Met	Leu	Arg	Leu	Asp	Thr	Leu	Gly	Ile	Arg	Ile	Leu	Lys	340	345	350
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His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	385	390	395
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Pro	Glu	Arg	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	435	440	445
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Phe	Arg	Leu	Pro	Lys	Trp	Met	Trp	Gln	Gly	Phe	Leu	Gly	Ser	Thr	Leu	465	470	475
Thr	Ser	Gly	Asp	Leu	Val	Leu	Phe	Ala	Leu	Tyr	Met	Phe	Val	Ile	Ser	485	490	495
Pro	Asn	Asn	Leu	Arg	Lys	Gly	Leu	Ile	Asn	His	Leu	Ile	Ser	Asp	Pro	500	505	510
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Ser Arg Arg Val Val Pro Arg Ala Val Glu Pro Arg Arg Arg Gly Arg	
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Trp Met Val Arg Cys Val Ala Thr Glu Lys His Lys Asp Ala Ala Ala	
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Lys Gly Gly Gly Gly Glu Leu Leu Tyr Val Gln Met Gln Ala Ser Lys	
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Ser Met Asp Ser Gln Ser Lys Ile Ser Ser Lys Leu Leu Pro Ile Pro	
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Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu	
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Lys Asp Thr Ile Val Tyr Leu Asp Gly Asn Lys Pro Ile Met Ile Gly	
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Lys Ile Met Glu Ser Pro Asp Gly His Arg Val Val Cys Cys Glu Gly	
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Ser Gly Arg Leu Leu Glu Tyr Glu Val Gly Gly Pro Arg Val Cys Val	
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Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn	Asn	Pro	Tyr	Asp	
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Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Cys	Phe	Lys	Asp	Lys	
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Phe	Ser	His	Pro	Glu	Gln	Gly	Asn	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	
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atg	tca	tcc	aca	cga	att	ttc	ttt	gag	gaa	aca	tgc	cta	gct	tct	aaa	1008
Met	Ser	Ser	Thr	Arg	Ile	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	
				325					330					335		
gaa	gca	atg	ccc	ttt	gac	ctc	ctt	aaa	aag	cgg	ttg	atg	tct	cgg	ttg	1056
Glu	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Arg	Leu	Met	Ser	Arg	Leu	
			340					345					350			
gat	gca	atg	gga	gtt	cat	att	cga	aaa	gta	tac	gag	gag	gaa	tgg	tcc	1104
Asp	Ala	Met	Gly	Val	His	Ile	Arg	Lys	Val	Tyr	Glu	Glu	Glu	Trp	Ser	
		355					360					365				
tac	att	cct	gtt	gga	ggg	tcc	tta	cca	aat	aca	gac	cag	aaa	aat	ctc	1152
Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Asp	Gln	Lys	Asn	Leu	
	370					375					380					
gca	ttt	ggc	gca	gca	agt	atg	gtg	cat	cct	gca	acc	gga	tac	tcg		1200
Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	
385					390					395				400		
gtg	gtt	aga	tca	ttg	tct	gaa	gct	cca	aga	tat	gca	tct	gtg	ata	tct	1248
Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Arg	Tyr	Ala	Ser	Val	Ile	Ser	
				405					410					415		
gat	atc	ttg	aga	aac	cgt	gtc	tac	cct	gga	gaa	tat	ttg	cct	gga	acc	1296
Asp	Ile	Leu	Arg	Asn	Arg	Val	Tyr	Pro	Gly	Glu	Tyr	Leu	Pro	Gly	Thr	
			420					425					430			
tct	caa	agt	tcc	agt	cca	tca	atg	ctt	gca	tgg	aga	aca	tta	tgg	ccc	1344
Ser	Gln	Ser	Ser	Ser	Pro	Ser	Met	Leu	Ala	Trp	Arg	Thr	Leu	Trp	Pro	
		435					440					445				
caa	gaa	cgg	aaa	cgt	caa	cga	tca	ttc	ttc	ctt	ttt	ggg	ctg	gct	ttg	1392
Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	
	450					455					460					
ata	atc	caa	ctg	aat	aac	gaa	ggc	att	cag	aca	ttc	ttt	gaa	acc	ttt	1440
Ile	Ile	Gln	Leu	Asn	Asn	Glu	Gly	Ile	Gln	Thr	Phe	Phe	Glu	Thr	Phe	
465					470					475					480	
ttc	cgg	ttg	ccc	aaa	tgg	atg	tgg	cga	gga	ttc	ctt	ggt	tcg	acg	ctt	1488
Phe	Arg	Leu	Pro	Lys	Trp	Met	Trp	Arg	Gly	Phe	Leu	Gly	Ser	Thr	Leu	
				485					490					495		
tct	tca	gtg	gat	ctc	ata	ctc	ttt	gca	ttc	tac	atg	ttc	aca	att	gcg	1536
Ser	Ser	Val	Asp	Leu	Ile	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Thr	Ile	Ala	
			500					505					510			
ccg	aac	caa	atg	cga	atg	aac	ctt	gtc	aga	cat	ctc	ctc	tct	gat	ccg	1584
Pro	Asn	Gln	Met	Arg	Met	Asn	Leu	Val	Arg	His	Leu	Leu	Ser	Asp	Pro	
		515					520					525				
acc	ggc	tca	acg	atg	atc	aag	acc	tac	ctg	acc	ttg	taa				1623
Thr	Gly	Ser	Thr	Met	Ile	Lys	Thr	Tyr	Leu	Thr	Leu					
	530					535					540					

<400> 16

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Arg	Ala	Ala	Trp 20	Gly	Ala	Ala	Ala	Ala	Gly 25	Ala	Gly	Ala	Glu 30	Gly	Arg
Ser	Arg	Arg 35	Val	Val	Pro	Arg	Ala 40	Val	Glu	Pro	Arg	Arg 45	Arg	Gly	Arg
Trp	Met 50	Val	Arg	Cys	Val	Ala 55	Thr	Glu	Lys	His	Lys 60	Asp	Ala	Ala	Ala
Arg 65	Arg	Gly	Gly	Val	Glu 70	Val	Glu	Phe	Ala	Asp 75	Glu	Glu	Asp	Tyr	Val 80
Lys	Gly	Gly	Gly	Gly 85	Glu	Leu	Leu	Tyr	Val 90	Gln	Met	Gln	Ala	Ser 95	Lys
Ser	Met	Asp	Ser 100	Gln	Ser	Lys	Ile	Ser 105	Ser	Lys	Leu	Leu 110	Pro	Ile	Pro
Asp	Glu	Asn 115	Ser	Val	Leu	Asp	Leu 120	Val	Ile	Ile	Gly	Cys 125	Gly	Pro	Ala
Gly 130	Leu	Ser	Leu	Ala	Ala 135	Glu	Ser	Ala	Lys	Lys	Gly 140	Leu	Asn	Val	Gly
Leu 145	Ile	Gly	Pro	Asp	Leu 150	Pro	Phe	Thr	Asn	Asn 155	Tyr	Gly	Val	Trp	Glu 160
Asp	Glu	Phe	Lys	Asp 165	Leu	Gly	Leu	Glu	Ser 170	Cys	Ile	Glu	His	Val 175	Trp
Lys	Asp	Thr 180	Ile	Val	Tyr	Leu	Asp	Gly 185	Asn	Lys	Pro	Ile	Met 190	Ile	Gly
Arg	Ala	Tyr 195	Gly	Arg	Val	His	Arg 200	Asp	Leu	Leu	His	Glu 205	Glu	Leu	Leu
Arg	Arg 210	Cys	Tyr	Asp	Ala	Gly 215	Val	Thr	Tyr	Leu	Ser 220	Ser	Lys	Val	Asp
Lys 225	Ile	Met	Glu	Ser	Pro 230	Asp	Gly	His	Arg	Val 235	Val	Cys	Cys	Glu	Gly 240
Asp	Arg	Glu	Val	Leu 245	Cys	Arg	Leu	Ala	Ile 250	Val	Ala	Ser	Gly	Ala 255	Ala
Ser	Gly	Arg	Leu 260	Leu	Glu	Tyr	Glu	Val 265	Gly	Gly	Pro	Arg	Val 270	Cys	Val
Gln	Thr 275	Ala	Tyr	Gly	Val	Glu	Val 280	Glu	Val	Glu	Asn 285	Asn	Pro	Tyr	Asp
Pro	Ser 290	Leu	Met	Val	Phe	Met 295	Asp	Tyr	Arg	Asp	Cys 300	Phe	Lys	Asp	Lys
Phe 305	Ser	His	Pro	Glu	Gln 310	Gly	Asn	Pro	Thr	Phe 315	Leu	Tyr	Ala	Met	Pro 320
Met	Ser	Ser	Thr	Arg 325	Ile	Phe	Phe	Glu	Glu 330	Thr	Cys	Leu	Ala	Ser 335	Lys
Glu	Ala	Met	Pro 340	Phe	Asp	Leu	Leu	Lys 345	Lys	Arg	Leu	Met	Ser 350	Arg	Leu

Asp	Ala	Met	Gly	Val	His	Ile	Arg	Lys	Val	Tyr	Glu	Glu	Glu	Trp	Ser	355	360	365	
Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Asp	Gln	Lys	Asn	Leu	370	375	380	
Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	385	390	395	400
Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Arg	Tyr	Ala	Ser	Val	Ile	Ser	405	410	415	
Asp	Ile	Leu	Arg	Asn	Arg	Val	Tyr	Pro	Gly	Glu	Tyr	Leu	Pro	Gly	Thr	420	425	430	
Ser	Gln	Ser	Ser	Ser	Pro	Ser	Met	Leu	Ala	Trp	Arg	Thr	Leu	Trp	Pro	435	440	445	
Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	450	455	460	
Ile	Ile	Gln	Leu	Asn	Asn	Glu	Gly	Ile	Gln	Thr	Phe	Phe	Glu	Thr	Phe	465	470	475	480
Phe	Arg	Leu	Pro	Lys	Trp	Met	Trp	Arg	Gly	Phe	Leu	Gly	Ser	Thr	Leu	485	490	495	
Ser	Ser	Val	Asp	Leu	Ile	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Thr	Ile	Ala	500	505	510	
Pro	Asn	Gln	Met	Arg	Met	Asn	Leu	Val	Arg	His	Leu	Leu	Ser	Asp	Pro	515	520	525	
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<211> 10

<212> PRT

<213> Artificial sequence

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<223> Description of the artificial sequence: protein motif for epsilon-cyclase

<220>

<221> VARIANT

<222> (2)

<223> G/C variation

<220>

<221> VARIANT

<222> (8)

<223> A/S variation

<220>

<221> VARIANT

<222> (9)

<223> V/L variation

<400> 17

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<210> 18

<211> 8

<212> PRT
<213> Artificial sequence
<220>
<223> Description of the artificial sequence: protein motif for epsilon-cyclase
<220>
<221> VARIANT
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<223> L/I variation
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<221> VARIANT
<222> (2)
<223> N/G/S variation
<220>
<221> VARIANT
<222> (7)
<223> K/R variation
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<221> VARIANT
<222> (8)
<223> V/L variation
<400> 18
Leu Asn Arg Xaa Tyr Gly Lys Val
1 5
<210> 19
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<212> PRT
<213> Artificial sequence
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<220>
<221> VARIANT
<222> (6)
<223> Y/W variation
<400> 19
Met Val Phe Met Asp Tyr Arg Asp
1 5
<210> 20
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<212> PRT
<213> Artificial sequence
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<223> Description of the artificial sequence: protein motif for epsilon-cyclase
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<221> VARIANT
<222> (6)
<223> A/V variation
<220>
<221> VARIANT

<222> (8)

<223> P/A variation

<400> 20

Pro Thr Phe Leu Tyr Ala Met Pro

1

5

<210> 21

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein motif for epsilon-cyclase

<220>

<221> VARIANT

<222> (7)

<223> S/A-variation

<220>

<221> VARIANT

<222> (11)

<223> M/S variation

<220>

<221> VARIANT

<222> (13)

<223> A/V variation

<400> 21

Ala Xaa Met Val His Pro Ser Thr Gly Tyr Met Val Ala Arg

1

5

10

<210> 22

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein motif for epsilon-cyclase

<220>

<221> VARIANT

<222> (7)

<223> R/K variation

<400> 22

Leu Trp Pro Xaa Glu Arg Arg Arg Gln Arg Xaa Phe Phe

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5

10

<210> 23

<211> 1780

<212> DNA

<213> Lactuca sativa

<220>

<221> CDS

<222> (77)..(1675)

<223> coding for epsilon-cyclase

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tgtgatagaa gaatca atg gag tgc ttt gga gct cga aac atg acg gca aca	112
Met Glu Cys Phe Gly Ala Arg Asn Met Thr Ala Thr	
1 5 10	
atg gcg gtt ttt acg tgc cct aga ttc acg gac tgt aat atc agg cac	160
Met Ala Val Phe Thr Cys Pro Arg Phe Thr Asp Cys Asn Ile Arg His	
15 20 25	
aaa ttt tcg tta ctg aaa caa cga aga ttt act aat tta tca gca tcg	208
Lys Phe Ser Leu Leu Lys Gln Arg Arg Phe Thr Asn Leu Ser Ala Ser	
30 35 40	
tct tcg ttg cgt caa att aag tgc agc gct aaa agc gac cgt tgt gta	256
Ser Ser Leu Arg Gln Ile Lys Cys Ser Ala Lys Ser Asp Arg Cys Val	
45 50 55 60	
gtg gat aaa caa ggg att tcc gta gca gac gaa gaa gat tat gtg aag	304
Val Asp Lys Gln Ile Ser Val Ala Asp Glu Glu Asp Tyr Val Lys	
65 70 75	
gcc ggt gga tcg gag ctg ttt ttt gtt caa atg cag cgg act aag tcc	352
Ala Gly Gly Ser Glu Leu Phe Phe Val Gln Met Gln Arg Thr Lys Ser	
80 85 90	
atg gaa agc cag tct aaa ctt tcc gaa aag cta gca cag ata cca att	400
Met Glu Ser Gln Ser Lys Leu Ser Glu Lys Leu Ala Gln Ile Pro Ile	
95 100 105	
gga aat tgc ata ctt gat ctg gtt gta atc ggt tgt ggc cct gct ggc	448
Gly Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly	
110 115 120	
ctt gct ctt gct gca gag tca gcc aaa cta ggg ttg aac gtt gga ctc	496
Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu	
125 130 135 140	
att ggc cct gat ctt cct ttt aca aac aat tat ggt gtt tgg cag gat	544
Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Gln Asp	
145 150 155	
gaa ttt ata ggt ctt gga ctt gaa gga tgc att gaa cat tct tgg aaa	592
Glu Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Ser Trp Lys	
160 165 170	
gat act ctt gta tac ctt gat gat gct gat ccc atc cgc ata ggt cgt	640
Asp Thr Leu Val Tyr Leu Asp Asp Ala Asp Pro Ile Arg Ile Gly Arg	
175 180 185	
gca tat ggc aga gtt cat cgt gat tta ctt cat gaa gag ttg tta aga	688
Ala Tyr Gly Arg Val His Arg Asp Leu Leu His Glu Glu Leu Leu Arg	
190 195 200	
agg tgt gtg gaa tca ggt gtt tca tat cta agc tcc aaa gta gaa aga	736
Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg	
205 210 215 220	
atc act gaa gct cca aat ggc tat agt ctc att gaa tgt gaa ggc aat	784
Ile Thr Glu Ala Pro Asn Gly Tyr Ser Leu Ile Glu Cys Glu Gly Asn	
225 230 235	
atc acc att cca tgc agg ctt gct act gtt gca tca ggg gca gct tca	832
Ile Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser	
240 245 250	
ggg aaa ttt ctg gag tat gaa ctt ggg ggt ccc cgt gtt tgt gtc caa	880
Gly Lys Phe Leu Glu Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln	
255 260 265	

aca gct tat ggt ata gag gtt gag gtt gaa aac aac ccc tat gat cca	928
Thr Ala Tyr Gly Ile Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro	
270 275 280	
gat cta atg gtg ttc atg gat tat aga gac ttc tca aaa cat aaa ccg	976
Asp Leu Met Val Phe Met Asp Tyr Arg Asp Phe Ser Lys His Lys Pro	
285 290 295 300	
gaa tct tta gaa gca aaa tat ccg act ttc ctc tat gtc atg gcc atg	1024
Glu Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu Tyr Val Met Ala Met	
305 310 315	
tct cca aca aaa ata ttc ttc gag gaa act tgt tta gct tca aga gaa	1072
Ser Pro Thr Lys Ile Phe Phe Glu Glu Thr Cys Leu Ala Ser Arg Glu	
320 325 330	
gcc atg cct ttc aat ctt cta aag tcc aaa ctc atg tca cga tta aag	1120
Ala Met Pro Phe Asn Leu Leu Lys Ser Lys Leu Met Ser Arg Leu Lys	
335 340 345	
gca atg ggt atc cga ata aca aga acg tac gaa gag gaa tgg tcg tat	1168
Ala Met Gly Ile Arg Ile Thr Arg Thr Tyr Glu Glu Glu Trp Ser Tyr	
350 355 360	
atc ccc gta ggt gga tcg tta cct aat aca gaa caa aag aat ctc gca	1216
Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala	
365 370 375 380	
ttt ggt gct gca gct agt atg gtg cac cct gcc aca ggg tat tca gtt	1264
Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val	
385 390 395	
gtt cga tct ttg tca gaa gct cct aat tat gca gca gtc att gct aag	1312
Val Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys	
400 405 410	
att tta aga caa gat caa tct aaa gag atg att tct ctt gga aaa tac	1360
Ile Leu Arg Gln Asp Gln Ser Lys Glu Met Ile Ser Leu Gly Lys Tyr	
415 420 425	
act aac att tca aaa caa gca tgg gaa aca ttg tgg cca ctt gaa agg	1408
Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg	
430 435 440	
aaa aga cag cga gcc ttc ttt cta ttc gga cta tca cac atc gtg cta	1456
Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ser His Ile Val Leu	
445 450 455 460	
atg gat cta gag gga aca cgt aca ttt ttc cgt act ttc ttt cgt ttg	1504
Met Asp Leu Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu	
465 470 475	
ccc aaa tgg atg tgg tgg gga ttt ttg ggg tct tct tta tct tca acg	1552
Pro Lys Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr	
480 485 490	
gat ttg ata ata ttt gcg ctt tat atg ttt gtg ata gca cct cac agc	1600
Asp Leu Ile Ile Phe Ala Leu Tyr Met Phe Val Ile Ala Pro His Ser	
495 500 505	
ttg aga atg gaa ctg gtt aga cat cta ctt tct gat ccg aca ggg gca	1648
Leu Arg Met Glu Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Ala	
510 515 520	
act atg gta aaa gca tat ctc act ata tagattttaga ttatataaat	1695
Thr Met Val Lys Ala Tyr Leu Thr Ile	
525 530	

1780

<213> Lactuca sativa

Ala Lys Tyr Pro Thr Phe Leu Tyr Val Met Ala Met Ser Pro Thr Lys
305 310 315 320

[illegible]

<210> 25

<211> 1848

<212> DNA

<213> Adonis palaestina

<220>

<221> CDS

<222> (116)..(1702)

<223> coding for epsilon cyclase

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Met
1

gaa cta ctt ggt gtt cgc aac ctc atc tct tct tgc cct gtc tgg act 166
Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp Thr
5 10 15

ttt gga aca aga aac ctt agt agt tca aaa cta gct tat aac ata cat 214
Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile His
20 25 30

cga	tat	ggg	tct	tct	tgt	aga	gta	gat	ttt	caa	gtg	agg	gct	gat	ggg	262
Arg	Tyr	Gly	Ser	Ser	Cys	Arg	Val	Asp	Phe	Gln	Val	Arg	Ala	Asp	Gly	
35						40					45					
gga	agc	ggg	agt	aga	act	tct	gtt	gct	tat	aaa	gag	ggg	ttt	gtg	gac	310
Gly	Ser	Gly	Ser	Arg	Thr	Ser	Val	Ala	Tyr	Lys	Glu	Gly	Phe	Val	Asp	
50					55					60					65	
gag	gag	gat	ttt	atc	aaa	gct	ggg	ggg	tct	gag	ctt	ttg	ttt	gtc	caa	358
Glu	Glu	Asp	Phe	Ile	Lys	Ala	Gly	Gly	Ser	Glu	Leu	Leu	Phe	Val	Gln	
				70					75					80		
atg	cag	caa	aca	aag	tct	atg	gag	aaa	cag	gcc	aag	ctc	gcc	gat	aag	406
Met	Gln	Gln	Thr	Lys	Ser	Met	Glu	Lys	Gln	Ala	Lys	Leu	Ala	Asp	Lys	
			85					90					95			
ttg	cca	cca	ata	cct	ttc	gga	gaa	tct	gtg	atg	gac	ttg	gtt	gta	ata	454
Leu	Pro	Pro	Ile	Pro	Phe	Gly	Glu	Ser	Val	Met	Asp	Leu	Val	Val	Ile	
	100						105					110				
ggg	tgt	gga	cct	gct	ggg	ctt	tca	ctg	gct	gca	gaa	gct	gct	aag	cta	502
Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ser	Leu	Ala	Ala	Glu	Ala	Ala	Lys	Leu	
	115					120					125					
ggc	ttg	aaa	gtt	ggc	ctt	att	ggg	cct	gat	ctt	cct	ttt	aca	aat	aat	550
Gly	Leu	Lys	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	
130					135					140					145	
tat	ggg	gtg	tgg	gaa	gac	gag	ttc	aaa	gat	ctt	gga	ctt	gaa	cgt	tgt	598
Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Glu	Arg	Cys	
				150					155					160		
atc	gag	cat	gct	tgg	aag	gac	acc	atc	gta	tat	ctt	gac	aat	gat	gct	646
Ile	Glu	His	Ala	Trp	Lys	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asn	Asp	Ala	
			165					170					175			
cct	gtc	ctt	att	ggg	cgt	gca	tat	gga	cga	gtt	agc	cgg	cat	ttg	ctg	694
Pro	Val	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Leu	Leu	
		180					185					190				
cat	gaa	gag	ttg	ctg	aaa	agg	tgt	gtc	gag	tca	ggg	gta	tca	tat	ctg	742
His	Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr	Leu	
	195					200					205					
aat	tct	aaa	gtg	gaa	agg	atc	act	gaa	gct	ggg	gat	ggc	cat	agt	ctt	790
Asn	Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala	Gly	Asp	Gly	His	Ser	Leu	
210					215					220					225	
gta	gtt	tgt	gaa	aac	gac	atc	ttt	atc	cct	tgc	agg	ctt	gct	act	gtt	838
Val	Val	Cys	Glu	Asn	Asp	Ile	Phe	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	
				230					235					240		
gca	tct	gga	gca	gct	tca	ggg	aaa	ctt	ttg	gag	tat	gaa	gta	ggg	ggc	886
Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu	Tyr	Glu	Val	Gly	Gly	
			245					250					255			
cct	cgt	gtt	tgt	gtc	caa	act	gct	tat	ggg	gtg	gag	gtt	gag	gtg	gag	934
Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	
		260					265					270				
aac	aat	cca	tac	gat	ccc	aac	tta	atg	gta	ttt	atg	gac	tac	aga	gac	982
Asn	Asn	Pro	Tyr	Asp	Pro	Asn	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	
	275					280					285					
tat	atg	caa	cag	aaa	tta	cag	tgc	tcg	gaa	gaa	gaa	tat	cca	aca	ttt	1030
Tyr	Met	Gln	Gln	Lys	Leu	Gln	Cys	Ser	Glu	Glu	Glu	Tyr	Pro	Thr	Phe	
290					295					300					305	

ctc tat gtc atg ccc atg tcg cca aca aga ctt ttt ttt gag gaa acc 1078
 Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu Thr
 310 315 320
 tgt ttg gcc tca aaa gat gcc atg cct ttc gat cta ctg aag aga aaa 1126
 Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg Lys
 325 330 335
 cta atg tca cga ttg aag act ctg ggt atc caa gtt aca aaa att tat 1174
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31

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<211> 1661

<212> DNA

<213> Arabidopsis thaliana

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Ser	Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	Pro	
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Gly	Leu	Arg	Met	Glu	Asp	Ile	Gln	Glu	Arg	Met	Ala	Ala	Arg	Leu	Lys	
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His	Leu	Gly	Ile	Asn	Val	Lys	Arg	Ile	Glu	Glu	Asp	Glu	Arg	Cys	Val	
			325					330					335			
atc	ccg	atg	ggc	ggt	cct	tta	cca	gtc	tta	cct	caa	cgg	gtt	gtg	ggg	1057
Ile	Pro	Met	Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val	Gly	
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Ile	Gly	Gly	Thr	Ala	Gly	Met	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	
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Ala	Arg	Thr	Leu	Ala	Ala	Ala	Pro	Ile	Val	Ala	Asn	Ala	Ile	Val	Arg	
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Tyr	Leu	Gly	Ser	Pro	Ser	Ser	Asn	Ser	Leu	Arg	Gly	Asp	Gln	Leu	Ser	
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Ala	Glu	Val	Trp	Arg	Asp	Leu	Trp	Pro	Ile	Glu	Arg	Arg	Arg	Gln	Arg	
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gag	ttc	ttc	tgt	ttt	gga	atg	gat	att	ctg	ctg	aaa	ctc	gat	tta	gac	1297
Glu	Phe	Phe	Cys	Phe	Gly	Met	Asp	Ile	Leu	Leu	Lys	Leu	Asp	Leu	Asp	
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35

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 Ala Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Gln Pro His Tyr
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 Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val
 450 455 460
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 Phe Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu
 465 470 475 480
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 Ile Met Thr Lys Gly Thr Val Pro Leu Ala Lys Met Ile Asn Asn Leu
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 gta caa gat aga gactaaggac cagaaactta gacatataag tatatctgtt 1541
 Val Gln Asp Arg
 500
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 Lys Glu Asn Leu Asp Phe Glu Leu Pro Leu Tyr Asp Thr Ser Lys Ser
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 Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr Thr Trp Ser
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 Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Leu Gln
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 Lys Cys Ile Thr Asn Gly Val Lys Phe His Gln Ser Lys Val Thr Asn
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 Val Val His Glu Glu Ala Asn Ser Thr Val Val Cys Ser Asp Gly Val
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36

Lys Ile Gln Ala Ser Val Val Leu Asp Ala Thr Gly Phe Ser Arg Cys
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 Gly Ile Ile Ala Glu Val Asp Gly His Pro Phe Asp Val Asp Lys Met
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 Val Phe Met Asp Trp Arg Asp Lys His Leu Asp Ser Tyr Pro Glu Leu
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 Lys Glu Arg Asn Ser Lys Ile Pro Thr Phe Leu Tyr Ala Met Pro Phe
 275 280 285
 Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg Pro
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 Gly Leu Arg Met Glu Asp Ile Gln Glu Arg Met Ala Ala Arg Leu Lys
 305 310 315 320
 His Leu Gly Ile Asn Val Lys Arg Ile Glu Glu Asp Glu Arg Cys Val
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 Ala Arg Thr Leu Ala Ala Ala Pro Ile Val Ala Asn Ala Ile Val Arg
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 Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val
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Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys	
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ttg gga tta aat gtt gga ctt att ggc ccg gat ctc cct ttc aca aac	200
Leu Gly Leu Asn Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn	
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aat tat ggt gtg tgg gaa gat gaa ttt aga gat ctt gga ctt gaa ggg	248
Asn Tyr Gly Val Trp Glu Asp Glu Phe Arg Asp Leu Gly Leu Glu Gly	
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Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Ile Asp Glu Asp	
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Glu Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu	
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Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser Tyr	
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ctt agc tca aaa gtg gaa agc att acg gaa tct acc agt ggt cat cgt	440
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Leu Val Ala Cys Glu His Asp Met Ile Val Pro Cys Arg Leu Ala Thr	
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Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly	
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Gly Pro Lys Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val	
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gac tgt act aag caa gaa gtt cca tct ttt gaa tct gac aat cca aca	680
Asp Cys Thr Lys Gln Glu Val Pro Ser Phe Glu Ser Asp Asn Pro Thr	
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Phe Leu Tyr Val Met Pro Met Ser Ser Thr Arg Val Phe Phe Glu Glu	
215 220 225	
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Thr Cys Leu Ala Ser Lys Asp Gly Leu Arg Phe Asp Ile Leu Lys Lys	
230 235 240	
aag ctc atg gca agg tta gag aga ttg gga atc cag gtt ttg aaa act	824
Lys Leu Met Ala Arg Leu Glu Arg Leu Gly Ile Gln Val Leu Lys Thr	
245 250 255 260	

38

tat gaa gag gaa tgg tca tat att cca gtt ggt ggt tcc tta cca aat 872
 Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
 265 270 275
 aca gaa caa aga aac ctc gca ttt ggt gct gct gct agc atg gtg cat 920
 Thr Glu Gln Arg Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
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 cca gcc act ggc tac tca gta gtc aga tca ctg tca gag gct cca aac 968
 Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Asn
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 Tyr Ala Ser Ala Ile Ala Tyr Ile Leu Lys His Asp His Ser Arg Gly
 310 315 320
 aga ctt aca cat gaa caa agt aat gag aat atc tca atg caa gct tgg 1064
 Arg Leu Thr His Glu Gln Ser Asn Glu Asn Ile Ser Met Gln Ala Trp
 325 330 335 340
 aat act ctc tgg cca cag gaa agg aag cgc caa aga gct ttt ttc ctc 1112
 Asn Thr Leu Trp Pro Gln Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
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 Phe Gly Leu Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Thr
 360 365 370
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 Phe Phe Arg Thr Phe Phe Arg Leu Pro Lys Trp Met Trp His Gly Phe
 375 380 385
 ctt ggt tct agt ctc tca tca gcc gat ctc att cta ttt gcc ttc tat 1256
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 Met Phe Ile Ile Ala Pro Asn Asp Leu Arg Lys Cys Leu Ile Arg His
 405 410 415 420
 cta gtt tca gat cca act gga gca act atg gta aga aca tac ctg act 1352
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 ttgccatacg tgacacataa tgagcttgta tatatactcc atgtatactg taaactgtta 1465
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Ile	Asp	Glu	Asp	Glu	Pro	Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val
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Ser	Arg	His	Leu	Leu	His	Glu	Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu	Ser
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Gly	Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Ser	Ile	Thr	Glu	Ser	Thr
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Arg	Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu
145					150					155					160
Tyr	Glu	Val	Gly	Gly	Pro	Lys	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val
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Glu	Val	Glu	Val	Glu	Asn	Asn	Pro	Tyr	Asp	Pro	Ser	Leu	Met	Val	Phe
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Met	Asp	Tyr	Arg	Asp	Cys	Thr	Lys	Gln	Glu	Val	Pro	Ser	Phe	Glu	Ser
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Asp	Asn	Pro	Thr	Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	Ser	Thr	Arg	Val
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Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	Asp	Gly	Leu	Arg	Phe	Asp
225					230					235					240
Ile	Leu	Lys	Lys	Lys	Leu	Met	Ala	Arg	Leu	Glu	Arg	Leu	Gly	Ile	Gln
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Ser	Leu	Pro	Asn	Thr	Glu	Gln	Arg	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala
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Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser
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His	Ser	Arg	Gly	Arg	Leu	Thr	His	Glu	Gln	Ser	Asn	Glu	Asn	Ile	Ser
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Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	Ile	Leu	Gln	Leu	Asp	Ile	Glu
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Gly	Ile	Arg	Thr	Phe	Phe	Arg	Thr	Phe	Phe	Arg	Leu	Pro	Lys	Trp	Met
	370					375					380				
Trp	His	Gly	Phe	Leu	Gly	Ser	Ser	Leu	Ser	Ser	Ala	Asp	Leu	Ile	Leu
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Phe	Ala	Phe	Tyr	Met											

Thr Tyr Leu Thr Leu
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Leu Asn Gly Val Thr Asp Asn Pro Cys Arg Lys Ala Met Asp Thr Leu
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ctc aaa act cat aac aag ctt gaa ttc ttg ccc caa gtt cac ggg gct 208
Leu Lys Thr His Asn Lys Leu Glu Phe Leu Pro Gln Val His Gly Ala
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ttg gaa aaa tcc agt agt tta agc tca ttg aag att cag aac cag gag 256
Leu Glu Lys Ser Ser Ser Leu Ser Ser Leu Lys Ile Gln Asn Gln Glu
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ctt agg ttt ggt ctc aag aag tct cgt caa aag agg aat agg agt tgt 304
Leu Arg Phe Gly Leu Lys Lys Ser Arg Gln Lys Arg Asn Arg Ser Cys
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ttc att aag gct agt agt agt gct ctt ttg gag cta gtt cct gaa acc 352
Phe Ile Lys Ala Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
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aag aag gaa aat ctt gaa ttt gag ctt ccc atg tat gac cca tca aag 400
Lys Lys Glu Asn Leu Glu Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
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gat gaa ttt gag gcc atg gat ttg ctt gat tgc ctt gat act act tgg 592
Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr Thr Trp
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Ser Gly Ala Val Val His Ile Asp Asp Asn Thr Lys Lys Asp Leu Asn
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aga cct tat ggg aga gtt aat agg aag ttg ctg aag tcg aaa atg ctg 688
Arg Pro Tyr Gly Arg Val Asn Arg Lys Leu Leu Lys Ser Lys Met Leu
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Lys	Val	Ile	His	Glu	Glu	Ser	Lys	Ser	Leu	Leu	Ile	Cys	Asn	Asp	Gly	
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Val	Thr	Ile	Gln	Ala	Ala	Val	Val	Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg	
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Cys	Leu	Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala	
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Val	Ile	Pro	Met	Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val	
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Gly	Ile	Gly	Gly	Thr	Ala	Gly	Met	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	
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Val	Ala	Arg	Thr	Leu	Ala	Ala	Ala	Pro	Ile	Val	Ala	Asn	Ala	Ile	Val	
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Arg	Ser	Leu	Ser	Ser	Asp	Arg	Ser	Ile	Ser	Gly	His	Lys	Leu	Ser	Ala	
	410				415						420					
gaa	gtt	tgg	aaa	gat	ttg	tgg	ccc	ata	gaa	agg	aga	agg	caa	agg	gag	1408
Glu	Val	Trp	Lys	Asp	Leu	Trp	Pro	Ile	Glu	Arg	Arg	Arg	Gln	Arg	Glu	
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ttc	ttc	tgt	ttt	ggg	atg	gat	atc	ctg	ctc	aaa	ctt	gac	tta	cct	gcc	1456
Phe	Phe	Cys	Phe	Gly	Met	Asp	Ile	Leu	Leu	Lys	Leu	Asp	Leu	Pro	Ala	
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act	agg	agg	ttt	ttc	gat	gct	ttt	ttt	gat	ctg	gag	cct	cgt	tat	tgg	1504
Thr	Arg	Arg	Phe	Phe	Asp	Ala	Phe	Phe	Asp	Leu	Glu	Pro	Arg	Tyr	Trp	
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His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val Phe
475 480 485
ggg ctt tct cta ttc tca cat gcc tct aat act tct agg cta gag atc 1600
Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu Ile
490 495 500
atg gca aag gga act ctt cct ttg gtt aac atg atc aac aac ttg gta 1648
Met Ala Lys Gly Thr Leu Pro Leu Val Asn Met Ile Asn Asn Leu Val
505 510 515 520
caa gat aca gat taaggtagacc atgatagtta taatgtgctt aataactcat 1700
Gln Asp Thr Asp
gcactaatcg ttataaaac acttcaaatt agttttgatg ttatagctt attacatgaa 1760
ccaaagctta tgatagacgt gcttttggtat ttaagagttt cagccaaaaa aaaaaaaaaa 1820
aaaaaaaaaa 1830
<210> 34
<211> 524
<212> PRT
<213> Citrus X paradisi
<400> 34
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Cys Arg Lys Ala Met Asp Thr Leu Leu Lys Thr His Asn Lys Leu Glu
20 25 30
Phe Leu Pro Gln Val His Gly Ala Leu Glu Lys Ser Ser Ser Leu Ser
35 40 45
Ser Leu Lys Ile Gln Asn Gln Glu Leu Arg Phe Gly Leu Lys Lys Ser
50 55 60
Arg Gln Lys Arg Asn Arg Ser Cys Phe Ile Lys Ala Ser Ser Ser Ala
65 70 75 80
Leu Leu Glu Leu Val Pro Glu Thr Lys Lys Glu Asn Leu Glu Phe Glu
85 90 95
Leu Pro Met Tyr Asp Pro Ser Lys Gly Leu Val Val Asp Leu Ala Val
100 105 110
Val Gly Gly Gly Pro Ala Gly Leu Ala Val Ala Gln Gln Val Ser Gly
115 120 125
Ala Gly Leu Ser Val Cys Ser Ile Asp Pro Ser Pro Lys Leu Ile Trp
130 135 140
Pro Asn Asn Tyr Gly Val Trp Val Asp Glu Phe Glu Ala Met Asp Leu
145 150 155 160
Leu Asp Cys Leu Asp Thr Thr Trp Ser Gly Ala Val Val His Ile Asp
165 170 175
Asp Asn Thr Lys Lys Asp Leu Asn Arg Pro Tyr Gly Arg Val Asn Arg
180 185 190
Lys Leu Leu Lys Ser Lys Met Leu Gln Lys Cys Ile Thr Asn Gly Val
195 200 205
Lys Phe His Gln Ala Lys Val Ile Lys Val Ile His Glu Glu Ser Lys
210 215 220
Ser Leu Leu Ile Cys Asn Asp Gly Val Thr Ile Gln Ala Ala Val Val
225 230 235 240

<210> 35

<212> DNA

<220>

<221> CDS

<222> (2) . . (787)

<223> coding for epsilon-cyclase (partial)

<400> 35

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Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu
1 5 10 15

44

att ggc ccg gat ctc cct ttc aca aac aat tat ggt gtg tgg gaa gat	97
Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp	
20 25 30	
gaa ttt aga gat ctt gga ctt gaa ggg tgt atc gaa caa gtc tgg aga	145
Glu Phe Arg Asp Leu Gly Leu Glu Gly Cys Ile Glu Gln Val Trp Arg	
35 40 45	
gac aca gtt gta tat att gat gaa gat gaa ccc atc ttg att ggt cgt	193
Asp Thr Val Val Tyr Ile Asp Glu Asp Glu Pro Ile Leu Ile Gly Arg	
50 55 60	
gct tat gga cga gtt agt cga cat ttg ctt cat gaa gaa tta tta aga	241
Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu Arg	
65 70 75 80	
agg tgt gtc gag tca ggt gta tca tat ctt agc tca aaa gtg gaa agc	289
Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Ser	
85 90 95	
att acg gaa tct acc agt ggt cat cgt ctt gta gct tgt gaa cat gat	337
Ile Thr Glu Ser Thr Ser Gly His Arg Leu Val Ala Cys Glu His Asp	
100 105 110	
atg att gtc ccc tgc agg ctt gct act gtt gct tct gga gca gca tca	385
Met Ile Val Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser	
115 120 125	
ggg aag cta ttg gaa tat ggg gtg ggg ggt ccc aaa gtt tct gtc caa	433
Gly Lys Leu Leu Glu Tyr Gly Val Gly Gly Pro Lys Val Ser Val Gln	
130 135 140	
aca gct tat ggt gtg gag gtt gag gtg gaa aat aat cca tat gat cca	481
Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro	
145 150 155 160	
agc ctt atg gtt ttc atg gac tac aga gac tgt act aag caa gaa gtt	529
Ser Leu Met Val Phe Met Asp Tyr Arg Asp Cys Thr Lys Gln Glu Val	
165 170 175	
cca tct ttt gaa tct gac aat cca aca ttt ctt tat gtc atg ccc atg	577
Pro Ser Phe Glu Ser Asp Asn Pro Thr Phe Leu Tyr Val Met Pro Met	
180 185 190	
tct tca aca aga gtt ttc ttt gag gaa act tgt ttg gca tcg aaa gat	625
Ser Ser Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Asp	
195 200 205	
ggc tta cgt ttt gac ata ttg aag aaa aag ctc atg gca agg tta gag	673
Gly Leu Arg Phe Asp Ile Leu Lys Lys Lys Leu Met Ala Arg Leu Glu	
210 215 220	
aga ttg gga atc cag gtt ttg aaa act tat gaa gag gaa tgg tca tat	721
Arg Leu Gly Ile Gln Val Leu Lys Thr Tyr Glu Glu Glu Trp Ser Tyr	
225 230 235 240	
att cca gtt ggt ggt tcc tta cca aat aca gaa caa aga aac ctc gca	769
Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Arg Asn Leu Ala	
245 250 255	
tat ggt gct gct gct agc	787
Tyr Gly Ala Ala Ala Ser	
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<210> 36

<211> 262

<212> PRT

<213> Citrus sinensis

<400> 36

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          20              25              30
Glu Phe Arg Asp Leu Gly Leu Glu Gly Cys Ile Glu Gln Val Trp Arg
          35              40              45
Asp Thr Val Val Tyr Ile Asp Glu Asp Glu Pro Ile Leu Ile Gly Arg
          50              55              60
Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu Arg
          65              70              75              80
Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Ser
          85              90              95
Ile Thr Glu Ser Thr Ser Gly His Arg Leu Val Ala Cys Glu His Asp
          100             105             110
Met Ile Val Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser
          115             120             125
Gly Lys Leu Leu Glu Tyr Gly Val Gly Gly Pro Lys Val Ser Val Gln
          130             135             140
Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro
          145             150             155             160
Ser Leu Met Val Phe Met Asp Tyr Arg Asp Cys Thr Lys Gln Glu Val
          165             170             175
Pro Ser Phe Glu Ser Asp Asn Pro Thr Phe Leu Tyr Val Met Pro Met
          180             185             190
Ser Ser Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Asp
          195             200             205
Gly Leu Arg Phe Asp Ile Leu Lys Lys Lys Leu Met Ala Arg Leu Glu
          210             215             220
Arg Leu Gly Ile Gln Val Leu Lys Thr Tyr Glu Glu Glu Trp Ser Tyr
          225             230             235             240
Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Arg Asn Leu Ala
          245             250             255
Tyr Gly Ala Ala Ala Ser
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<210> 37

<211> 2357

<212> DNA

<213> Spinacia oleracea

<220>

<221> CDS

<222> (264)..(1814)

<223> coding for epsilon-cyclase

<400> 37

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cactgaactt caccactaca aacttaaaaa aaatcttggg gaaatttgat tccgtaaaaa 180
tggagtatta ttgtctcgga gcttcgaaat tcgcaacaat ggcggtttct cctgcgctta 240
atcacgacaa tttgaggaat aaa atg gtt aaa caa cgc cag aat ttc cag acg 293
Met Val Lys Gln Arg Gln Asn Phe Gln Thr
      1              5              10
ttt tgc ttt tgg agg ccg aat tct tcg aac gtt gta gta gaa tgt agt 341
Phe Cys Phe Trp Arg Pro Asn Ser Ser Asn Val Val Val Glu Cys Ser
      15              20              25
agt cgt agg agt gga agt agt gtt ttg agg agt gcg aat agc gac agt 389
Ser Arg Arg Ser Gly Ser Ser Val Leu Arg Ser Ala Asn Ser Asp Ser
      30              35              40
agt tgc gta att gcg cca gag gat ttt gcg aac gaa gaa gat ttc atc 437
Ser Cys Val Ile Ala Pro Glu Asp Phe Ala Asn Glu Glu Asp Phe Ile
      45              50              55
aaa gct ggt ggt tcc gag ctt ctt tat gtt caa atg cag cag aat aaa 485
Lys Ala Gly Gly Ser Glu Leu Leu Tyr Val Gln Met Gln Gln Asn Lys
      60              65              70
gct atg gat tgt tac tcc aaa att tcc gat aag ctg cgt caa ata tca 533
Ala Met Asp Cys Tyr Ser Lys Ile Ser Asp Lys Leu Arg Gln Ile Ser
      75              80              85              90
gat gcc aat gaa ctg ctg gat atg gtg gtt att ggt tgt ggt cca gct 581
Asp Ala Asn Glu Leu Leu Asp Met Val Val Ile Gly Cys Gly Pro Ala
      95              100              105
ggt cta gct ttg gct gca gaa tcg gct aaa ctt gga tta aaa gtt ggc 629
Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu Lys Val Gly
      110              115              120
ctt gtt ggt cct gat ctt cct ttt acg aat aac tac ggc gtt tgg gaa 677
Leu Val Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu
      125              130              135
gat gaa ttc aga gca ttg gga ctt gga ggc tgt atc gag cac gtt tgg 725
Asp Glu Phe Arg Ala Leu Gly Leu Gly Gly Cys Ile Glu His Val Trp
      140              145              150
cgt gat acc att gtg tat att gat gat gac aat cct ata tat att ggt 773
Arg Asp Thr Ile Val Tyr Ile Asp Asp Asp Asn Pro Ile Tyr Ile Gly
      155              160              165              170
cga tct tat gga aaa gtc agc cgg caa tta ctt cac aag gaa ctg gtg 821
Arg Ser Tyr Gly Lys Val Ser Arg Gln Leu Leu His Lys Glu Leu Val
      175              180              185
cac agg tgt ttg gag tca ggt gtc tct tat ctg aat gcg aaa gtg gaa 869
His Arg Cys Leu Glu Ser Gly Val Ser Tyr Leu Asn Ala Lys Val Glu
      190              195              200
aat att atg gaa gga cct gat gga cat agg ctt gtt gct tgt gaa cgt 917
Asn Ile Met Glu Gly Pro Asp Gly His Arg Leu Val Ala Cys Glu Arg
      205              210              215
ggt gtc act att ccc tgc agg ctt gta act gtt gca tct gga gca gct 965
Gly Val Thr Ile Pro Cys Arg Leu Val Thr Val Ala Ser Gly Ala Ala
      220              225              230
tca ggg aaa ctt ctg gag tat gaa gtg ggt ggt cca agg gtt tgt gta 1013
Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly Gly Pro Arg Val Cys Val
      235              240              245              250

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caa aca gct tat ggt gtg gag gtg gag gtg gaa aac agt cct tat gat	1061
Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Ser Pro Tyr Asp	
255 260 265	
ccc aat gtg atg gtg ttc atg gac tac aga gac tac act aaa ctg agc	1109
Pro Asn Val Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys Leu Ser	
270 275 280	
gtt caa tct ctg gag gca aag tat cca aca ttc ttg tat gca atg ccg	1157
Val Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu Tyr Ala Met Pro	
285 290 295	
ata tca cca act agg atc ttc ttt gag gag act tgc ttg gct tca gta	1205
Ile Ser Pro Thr Arg Ile Phe Phe Glu Glu Thr Cys Leu Ala Ser Val	
300 305 310	
gat gca atg ccc ttt gac ctg ctc aag aaa aag ctt atg aca aga tta	1253
Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met Thr Arg Leu	
315 320 325 330	
caa act atg ggt gtt cgt atc acc aaa ata tat gaa gag gag tgg tct	1301
Gln Thr Met Gly Val Arg Ile Thr Lys Ile Tyr Glu Glu Glu Trp Ser	
335 340 345	
tat ata cct gtt ggt ggg tcc tta cca aat aca gag caa aga aac ctt	1349
Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Arg Asn Leu	
350 355 360	
gca ttt ggt gct gct gcg agc atg gtg cat cca gcc aca ggt tat tca	1397
Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser	
365 370 375	
gtc gtg aga tca ctg tca gaa gct cca aag tat gct tct gca att gca	1445
Val Val Arg Ser Leu Ser Glu Ala Pro Lys Tyr Ala Ser Ala Ile Ala	
380 385 390	
aac ttg atc aag aat gac ctg tca aaa aat gca ata ttg cgt cag agg	1493
Asn Leu Ile Lys Asn Asp Leu Ser Lys Asn Ala Ile Leu Arg Gln Arg	
395 400 405 410	
agt gtg ggg aat atc tca atg caa gcc tgg aat act ctt tgg cca caa	1541
Ser Val Gly Asn Ile Ser Met Gln Ala Trp Asn Thr Leu Trp Pro Gln	
415 420 425	
gaa agg aaa cgt cag aga gca ttc ttc ctg ttc gga cta tca ctt ata	1589
Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ser Leu Ile	
430 435 440	
gtc cag ctt gat att gag ggt atc agg aca ttc ttc cgc acc ttc ttc	1637
Val Gln Leu Asp Ile Glu Gly Ile Arg Thr Phe Phe Arg Thr Phe Phe	
445 450 455	
cga gtg cca aaa tgg atg tgg gag gga ttc ctc ggt tct aat ctc tct	1685
Arg Val Pro Lys Trp Met Trp Glu Gly Phe Leu Gly Ser Asn Leu Ser	
460 465 470	
tca gct gat ctc ata ttg ttt gcc ttt tat atg ttc ttt att gct ccg	1733
Ser Ala Asp Leu Ile Leu Phe Ala Phe Tyr Met Phe Phe Ile Ala Pro	
475 480 485 490	
aat gac ttg aga atg ggt ctt ata agg cat cta cta tct gat cct aca	1781
Asn Asp Leu Arg Met Gly Leu Ile Arg His Leu Leu Ser Asp Pro Thr	
495 500 505	
ggg gcg acc atg ata aga acg tac ata aca cta taaaagtaat atgaaatgct	1834
Gly Ala Thr Met Ile Arg Thr Tyr Ile Thr Leu	
510 515	

cactcctttg tacatcatgc aaaattggta cgaattgact ggactatgca gtctaacttg 1894
 gtgtaaaaaa aacacaatta ataaattttt tgtagggtgca gcctctatac ttgatattct 1954
 cgattcagat ataattattgt cagtattctt cgtaaagat cagttgtttc tacaattcca 2014
 gaggtcctg gaattggtgt tacccttcca tgtagctcat tgataaatgt tgagggtaga 2074
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 atcacagggt agccagctca actacgtagg tcaaccttga gccactccca aacatttttg 2254
 cagctgatgg gggtcaccct gtaaggtagag tttcttacca actccaccaa cttatgttgg 2314
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<210> 38

<211> 517

<212> PRT

<213> *Spinacia oleracea*

<400> 38

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Asn	Ser	Ser	Asn	Val	Val	Val	Glu	Cys	Ser	Ser	Arg	Arg	Ser	Gly	Ser	20	25	30	
Ser	Val	Leu	Arg	Ser	Ala	Asn	Ser	Asp	Ser	Ser	Cys	Val	Ile	Ala	Pro	35	40	45	
Glu	Asp	Phe	Ala	Asn	Glu	Glu	Asp	Phe	Ile	Lys	Ala	Gly	Gly	Ser	Glu	50	55	60	
Leu	Leu	Tyr	Val	Gln	Met	Gln	Gln	Asn	Lys	Ala	Met	Asp	Cys	Tyr	Ser	65	70	75	80
Lys	Ile	Ser	Asp	Lys	Leu	Arg	Gln	Ile	Ser	Asp	Ala	Asn	Glu	Leu	Leu	85	90	95	
Asp	Met	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	100	105	110	
Glu	Ser	Ala	Lys	Leu	Gly	Leu	Lys	Val	Gly	Leu	Val	Gly	Pro	Asp	Leu	115	120	125	
Pro	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Arg	Ala	Leu	130	135	140	
Gly	Leu	Gly	Gly	Cys	Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	145	150	155	160
Ile	Asp	Asp	Asp	Asn	Pro	Ile	Tyr	Ile	Gly	Arg	Ser	Tyr	Gly	Lys	Val	165	170	175	
Ser	Arg	Gln	Leu	Leu	His	Lys	Glu	Leu	Val	His	Arg	Cys	Leu	Glu	Ser	180	185	190	
Gly	Val	Ser	Tyr	Leu	Asn	Ala	Lys	Val	Glu	Asn	Ile	Met	Glu	Gly	Pro	195	200	205	
Asp	Gly	His	Arg	Leu	Val	Ala	Cys	Glu	Arg	Gly	Val	Thr	Ile	Pro	Cys	210	215	220	
Arg	Leu	Val	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu	225	230	235	240
Tyr	Glu	Val	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	245	250	255	


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<210> 39
<211> 1378
<212> DNA
<213> Solanum tuberosum
<220>
<221> CDS
<222> (2)..(1147)
<223> coding for episilon-cyclase (partial)
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  Ser Xaa Xaa Xaa Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile
    1             5             10             15
gaa cat gtt tgg cgg gat acc att gta tat ctt gat gat gat gat cct 97
Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Asp Pro
    20             25             30

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50

att ctt att ggc cgt gcc tat gga aga gtt agt cgc cat tta ctg cac	145
Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His	
35 40 45	
gag gag tta ctc aaa agg tgt gtg gag gca ggt gtt ttg tat cta aac	193
Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn	
50 55 60	
tcg aaa gtg gat agg att gtt gag gcc aca aat ggc cac agt ctt gta	241
Ser Lys Val Asp Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val	
65 70 75 80	
gag tgc gag ggt gat gtt gtg att ccc tgc agg ttt gtg act gtt gca	289
Glu Cys Glu Gly Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala	
85 90 95	
tcg gga gca gcc tcg ggg aaa ttc ttg cag tat gag ttg gga ggt cct	337
Ser Gly Ala Ala Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro	
100 105 110	
aga gtt tct gtt caa aca gct tat gga gtg gaa gtt gag gtc gat aac	385
Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn	
115 120 125	
aat cca ttt gac ccg agc ctg atg gtt ttc atg gat tat aga gac tat	433
Asn Pro Phe Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr	
130 135 140	
gtc aga cac gac gct caa tct tta gaa gct aaa tat cca aca ttt ctc	481
Val Arg His Asp Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu	
145 150 155 160	
tat gcc atg ccc atg tct cca aca cga gtc ttt ttc gag gaa act tgt	529
Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys	
165 170 175	
ttg gct tca aaa gat gca atg cca ttc gat ctg tta aag aaa aaa ttg	577
Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu	
180 185 190	
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Met Leu Arg Leu Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu	
195 200 205	
gag gaa tgg tct tac ata cca gtt gga gga tct ttg cca aat aca gaa	673
Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu	
210 215 220	
caa aaa aca ctt gca ttt ggt gct gct gct agc atg gtt cat cca gcc	721
Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala	
225 230 235 240	
aca ggt tat tca gtc gtc aga tca ctg tct gaa gct cca aaa tgc gcc	769
Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala	
245 250 255	
ttc gtg ctt gca aat ata tta cga caa aat cat agc aag aat atg ctt	817
Phe Val Leu Ala Asn Ile Leu Arg Gln Asn His Ser Lys Asn Met Leu	
260 265 270	
act agt tca agt acc ccg agt att tca act caa gct tgg aac act ctt	865
Thr Ser Ser Ser Thr Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu	
275 280 285	
tgg cca caa gaa cga aaa cga caa aga tcg ttt ttc cta ttt gga ctg	913
Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu	
290 295 300	

51

gct ctg ata ttg cag ctg gat att gag ggg ata agg tca ttt ttc cgc 961
 Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg
 305 310 315 320
 gcg ttc ttc cgt gtg cca aaa tgg atg tgg cag gga ttt ctt ggt tca 1009
 Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser
 325 330 335
 agt ctt tct tna gca gac ctc atg tta ttt gcc ttc tac atg ttt att 1057
 Ser Leu Ser Xaa Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile
 340 345 350
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 Ile Ala Pro Asn Asp Met Arg Arg Gly Leu Ile Arg His Leu Leu Ser
 355 360 365
 gat cct act ggt gca aca ttg ata aga act tat ctt aca ttt 1147
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 <213> Solanum tuberosum
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 Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn
 50 55 60
 Ser Lys Val Asp Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val
 65 70 75 80
 Glu Cys Glu Gly Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala
 85 90 95
 Ser Gly Ala Ala Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro
 100 105 110
 Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn
 115 120 125
 Asn Pro Phe Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr
 130 135 140
 Val Arg His Asp Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu
 145 150 155 160
 Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys
 165 170 175
 Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu
 180 185 190

52

Met	Leu	Arg	Leu	Asn	Thr	Leu	Gly	Val	Arg	Ile	Lys	Glu	Ile	Tyr	Glu
		195					200					205			
Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu
	210					215					220				
Gln	Lys	Thr	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala
225					230					235					240
Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Cys	Ala
				245					250					255	
Phe	Val	Leu	Ala	Asn	Ile	Leu	Arg	Gln	Asn	His	Ser	Lys	Asn	Met	Leu
			260					265					270		
Thr	Ser	Ser	Ser	Thr	Pro	Ser	Ile	Ser	Thr	Gln	Ala	Trp	Asn	Thr	Leu
		275					280					285			
Trp	Pro	Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu
	290					295					300				
Ala	Leu	Ile	Leu	Gln	Leu	Asp	Ile	Glu	Gly	Ile	Arg	Ser	Phe	Phe	Arg
305					310					315					320
Ala	Phe	Phe	Arg	Val	Pro	Lys	Trp	Met	Trp	Gln	Gly	Phe	Leu	Gly	Ser
				325					330					335	
Ser	Leu	Ser	Xaa	Ala	Asp	Leu	Met	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Ile
			340					345					350		
Ile	Ala	Pro	Asn	Asp	Met	Arg	Arg	Gly	Leu	Ile	Arg	His	Leu	Leu	Ser
		355				360						365			
Asp	Pro	Thr	Gly	Ala	Thr	Leu	Ile	Arg	Thr	Tyr	Leu	Thr	Phe		
	370					375					380				

<210> 41

<211> 497

<212> DNA

<213> Daucus carota

<220>

<221> CDS

<222> (1)..(495)

<223> coding for episilon-cyclase (partial)

<400> 41

tat	ggt	ggt	tgg	gtg	gat	gaa	ttt	ata	gat	ctt	gga	ctt	gaa	ggg	tgt	48
Tyr	Gly	Val	Trp	Val	Asp	Glu	Phe	Ile	Asp	Leu	Gly	Leu	Glu	Gly	Cys	
1				5					10					15		
att	gag	cat	gtt	tgg	cgg	gat	act	att	gta	tat	ctt	gat	gat	ggg	gat	96
Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Gly	Asp	
			20					25					30			
cct	att	atg	att	ggc	cgt	gct	tac	gga	aga	gtt	agt	cgc	cat	ttg	ctt	144
Pro	Ile	Met	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Leu	Leu	
		35				40						45				
cat	gaa	gaa	ttg	ctt	aaa	agg	tgt	gtc	gag	tca	ggg	gtt	tcg	tat	ctt	192
His	Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr	Leu	
	50					55					60					
agc	tca	aaa	gtt	gaa	aag	att	att	gaa	gct	gga	gat	ggc	cac	agc	ctg	240
Ser	Ser	Lys	Val	Glu	Lys	Ile	Ile	Glu	Ala	Gly	Asp	Gly	His	Ser	Leu	
	65				70					75					80	

53

```

gtt gag tgt gaa aat aat att gtc att cca tgc agg ctt gct act gtt 288
Val Glu Cys Glu Asn Asn Ile Val Ile Pro Cys Arg Leu Ala Thr Val
                        85                      90                      95

gca tct gga gca gct tct ggg aaa ctt ttg cag tat gag gtt ggg ggt 336
Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly
                        100                      105                      110

ccc aga gtt tct gtc caa aca gct tat ggt gtc gag gtt gag gtg gaa 384
Pro Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu
                        115                      120                      125

aac aat cca tat gat ccc agt cta atg gtt ttc atg gat tac aga gat 432
Asn Asn Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp
                        130                      135                      140

tat acc aaa caa aaa gtt cca ggc atg gag gca gaa tat cca act ttc 480
Tyr Thr Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe
145                      150                      155                      160

ctg tat gcc atg cca tt
Leu Tyr Ala Met Pro
                        165

```

<210> 42

<211> 165

<212> PRT

<213> Daucus carota

<400> 42

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Tyr Gly Val Trp Val Asp Glu Phe Ile Asp Leu Gly Leu Glu Gly Cys
 1                      5                      10                      15

Ile Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Gly Asp
                20                      25                      30

Pro Ile Met Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu
 35                      40                      45

His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr Leu
 50                      55                      60

Ser Ser Lys Val Glu Lys Ile Ile Glu Ala Gly Asp Gly His Ser Leu
 65                      70                      75                      80

Val Glu Cys Glu Asn Asn Ile Val Ile Pro Cys Arg Leu Ala Thr Val
                        85                      90                      95

Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly
100                      105                      110

Pro Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu
115                      120                      125

Asn Asn Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp
130                      135                      140

Tyr Thr Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe
145                      150                      155                      160

Leu Tyr Ala Met Pro
                        165

```

<210> 43

<211> 605

<212> DNA

<213> Daucus carota

<220>

<221> CDS

<222> (3)..(605)

<223> coding for epsilon-cyclase (partial)

<400> 43

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tc att ggc cgt gct tat gga aga tta gtc gcc att tgc ttc atg aag      47
  Ile Gly Arg Ala Tyr Gly Arg Leu Val Ala Ile Cys Phe Met Lys
    1             5             10             15

aat tgc tta aaa ggt gtg tcg agt cag gtg ttt cgt atc tta gct caa      95
Asn Cys Leu Lys Gly Val Ser Ser Gln Val Phe Arg Ile Leu Ala Gln
                20             25             30

aag ttg aaa aga tta ttg aag ctg gag atg gcc aca gcc tgg ttg agt     143
Lys Leu Lys Arg Leu Leu Lys Leu Glu Met Ala Thr Ala Trp Leu Ser
                35             40             45

gtg aaa ata ata ttg tca ttc cat gca ggc ttg cta ctg ttg cat ctg     191
Val Lys Ile Ile Leu Ser Phe His Ala Gly Leu Leu Leu Leu His Leu
                50             55             60

gag cag ctt ctg gga aac ttt tgc agt atg ggg ttg ggg gtc cca gag     239
Glu Gln Leu Leu Gly Asn Phe Cys Ser Met Gly Leu Gly Val Pro Glu
                65             70             75

ttt ctg tcc aaa cag ctt atg gtg tcg agg ttg agg tgg aaa cca atc     287
Phe Leu Ser Lys Gln Leu Met Val Ser Arg Leu Arg Trp Lys Pro Ile
                80             85             90             95

cca tat gat ccc agt cta atg gtt ttc atg gat tac aga gat tat acc     335
Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr
                100            105            110

aaa caa aaa gtt cca ggc atg gag gca gaa tat cca aca ttt ctt tat     383
Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe Leu Tyr
                115            120            125

gtg atg ccc atg tcc cca aca agg att ttc ttt gag gag aca tgt ttg     431
Val Met Pro Met Ser Pro Thr Arg Ile Phe Phe Glu Glu Thr Cys Leu
                130            135            140

gct tca aaa gat gcg atg cca ttc gat cta ctg aag aaa aaa ctc atg     479
Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met
                145            150            155

tca aga tta cag acg atg gga att cga gtt gcc aag aca tat gaa gag     527
Ser Arg Leu Gln Thr Met Gly Ile Arg Val Ala Lys Thr Tyr Glu Glu
                160            165            170            175

gaa tgg tct tat ata cct gtt ggg gga tct tta cct aat act gag caa     575
Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln
                180            185            190

aag aat ctc gcc ttt ggt gct gcc gct aga                               605
Lys Asn Leu Ala Phe Gly Ala Ala Ala Arg
                195            200

```

<210> 44

<211> 201

<212> PRT

<213> Daucus carota

<400> 44

```

Ile Gly Arg Ala Tyr Gly Arg Leu Val Ala Ile Cys Phe Met Lys Asn
  1             5             10             15

```

55

Cys Leu Lys Gly Val Ser Ser Gln Val Phe Arg Ile Leu Ala Gln Lys
 20 25 30
 Leu Lys Arg Leu Leu Lys Leu Glu Met Ala Thr Ala Trp Leu Ser Val
 35 40 45
 Lys Ile Ile Leu Ser Phe His Ala Gly Leu Leu Leu Leu His Leu Glu
 50 55 60
 Gln Leu Leu Gly Asn Phe Cys Ser Met Gly Leu Gly Val Pro Glu Phe
 65 70 75 80
 Leu Ser Lys Gln Leu Met Val Ser Arg Leu Arg Trp Lys Pro Ile Pro
 85 90 95
 Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys
 100 105 110
 Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe Leu Tyr Val
 115 120 125
 Met Pro Met Ser Pro Thr Arg Ile Phe Phe Glu Glu Thr Cys Leu Ala
 130 135 140
 Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met Ser
 145 150 155 160
 Arg Leu Gln Thr Met Gly Ile Arg Val Ala Lys Thr Tyr Glu Glu Glu
 165 170 175
 Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys
 180 185 190
 Asn Leu Ala Phe Gly Ala Ala Ala Arg
 195 200

<210> 45

<211> 1697

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (6)..(1583)

<223> coding for epsilon-cyclase

<400> 45

ttgaa atg gag tgt gtt gga gtt caa aat gtt gga gca atg gca gtt tta 50
 Met Glu Cys Val Gly Val Gln Asn Val Gly Ala Met Ala Val Leu
 1 5 10 15
 acg cgt ccg aga ttg aac cgt tgg tcg gga gga gag tta tgc caa gaa 98
 Thr Arg Pro Arg Leu Asn Arg Trp Ser Gly Gly Glu Leu Cys Gln Glu
 20 25 30
 aaa agc atc ttt ttg gcg tat gag cag tat gaa agt aaa tgt aat agc 146
 Lys Ser Ile Phe Leu Ala Tyr Glu Gln Tyr Glu Ser Lys Cys Asn Ser
 35 40 45
 agt agt ggt agt gac agt tgt gta gtt gat aaa gaa gat ttt gct gat 194
 Ser Ser Gly Ser Asp Ser Cys Val Val Asp Lys Glu Asp Phe Ala Asp
 50 55 60
 gaa gaa gat tat ata aaa gcc ggt ggt tcg caa ctt gta ttt gtt caa 242
 Glu Glu Asp Tyr Ile Lys Ala Gly Gly Ser Gln Leu Val Phe Val Gln
 65 70 75

56

atg	cag	cag	aaa	aaa	gat	atg	gat	cag	cag	tct	aag	ctt	tct	gat	gag	290
Met	Gln	Gln	Lys	Lys	Asp	Met	Asp	Gln	Gln	Ser	Lys	Leu	Ser	Asp	Glu	
80					85					90					95	
tta	cga	caa	ata	tct	gct	gga	caa	acc	gta	ctg	gat	tta	gtg	gta	atc	338
Leu	Arg	Gln	Ile	Ser	Ala	Gly	Gln	Thr	Val	Leu	Asp	Leu	Val	Val	Ile	
			100						105					110		
ggc	tgt	ggt	cct	gct	ggt	ctt	gct	ctt	gcc	gcg	gag	tca	gct	aaa	ttg	386
Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	
			115					120					125			
ggg	ttg	aac	gtg	ggg	ctc	gtt	ggg	cct	gat	ctt	cct	ttc	aca	aac	aac	434
Gly	Leu	Asn	Val	Gly	Leu	Val	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	
		130					135					140				
tat	ggt	gta	tgg	gag	gac	gag	ttc	aaa	gat	ctt	ggt	ctt	caa	gcc	tgc	482
Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Gln	Ala	Cys	
	145					150					155					
att	gaa	cat	gtt	tgg	cgg	gat	acc	att	gta	tat	ctt	gat	gat	gat	gaa	530
Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Asp	Glu	
160					165				170						175	
cct	att	ctt	att	ggc	cgt	gcc	tat	gga	aga	gtt	agt	cgc	cat	ttt	ctg	578
Pro	Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Phe	Leu	
				180				185						190		
cac	gag	gag	tta	ctc	aaa	agg	tgt	gtg	gag	gca	ggt	gtt	ttg	tat	cta	626
His	Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ala	Gly	Val	Leu	Tyr	Leu	
			195					200					205			
aac	tcg	aaa	gtg	gat	agg	att	gtt	gag	gcc	aca	aat	ggc	cag	agt	ctt	674
Asn	Ser	Lys	Val	Asp	Arg	Ile	Val	Glu	Ala	Thr	Asn	Gly	Gln	Ser	Leu	
		210					215					220				
gta	gag	tgc	gaa	ggt	gat	gtt	gtg	att	ccc	tgc	agg	ttt	gtg	act	gtt	722
Val	Glu	Cys	Glu	Gly	Asp	Val	Val	Ile	Pro	Cys	Arg	Phe	Val	Thr	Val	
	225				230					235						
gca	tcg	ggg	gca	gcc	tcg	ggg	aaa	ttc	ttg	cag	tat	gag	ttg	gga	agt	770
Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu	Gln	Tyr	Glu	Leu	Gly	Ser	
240				245				250							255	
cct	aga	gtt	tct	gtt	caa	aca	gct	tat	gga	gtg	gaa	gtt	gag	gtt	gat	818
Pro	Arg	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Asp	
				260				265						270		
aac	aat	cca	ttt	gac	ccg	agc	ctg	atg	gtt	ttc	atg	gat	tat	aga	gat	866
Asn	Asn	Pro	Phe	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	
			275				280					285				
tat	ctc	aga	cac	gac	gct	caa	tct	tta	gaa	gct	aaa	tat	cca	aca	ttt	914
Tyr	Leu	Arg	His	Asp	Ala	Gln	Ser	Leu	Glu	Ala	Lys	Tyr	Pro	Thr	Phe	
		290					295					300				
ctt	tat	gcc	atg	ccc	atg	tct	cca	aca	cga	gtc	ttt	ttc	gag	gaa	act	962
Leu	Tyr	Ala	Met	Pro	Met	Ser	Pro	Thr	Arg	Val	Phe	Phe	Glu	Glu	Thr	
	305					310					315					
tgt	ttg	gct	tca	aaa	gat	gca	atg	cca	ttc	gat	ctg	tta	aag	aaa	aaa	1010
Cys	Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Lys	
320					325				330						335	
ctg	atg	cta	cga	ttg	aac	acc	ctt	ggt	gta	aga	att	aaa	gaa	att	tac	1058
Leu	Met	Leu	Arg	Leu	Asn	Thr	Leu	Gly	Val	Arg	Ile	Lys	Glu	Ile	Tyr	
				340					345						350	

57

gag gag gaa tgg tct tac ata ccg gtt ggt gga tct ttg cca aat aca 1106
 Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr
 355 360 365

gaa caa aaa aca ctt gca ttt ggt gct gct gct agc atg gtt cat cca 1154
 Glu Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro
 370 375 380

gcc aca ggt tat tca gtc gtc aga tca ctt tct gaa gct cca aaa tgc 1202
 Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys
 385 390 395

gcc tct gta ctt gca aat ata tta cga caa cat tat agc aag aac atg 1250
 Ala Ser Val Leu Ala Asn Ile Leu Arg Gln His Tyr Ser Lys Asn Met
 400 405 410 415

ctt acc agt tca agt atc ccg agt ata tca act caa gct tgg aac act 1298
 Leu Thr Ser Ser Ser Ile Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr
 420 425 430

ctt tgg cca caa gaa cga aaa cga caa aga tcg ttt ttc cta ttt gga 1346
 Leu Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly
 435 440 445

ctg gct ctg ata ttg cag ctg gat att gag ggg ata agg tca ttt ttc 1394
 Leu Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe
 450 455 460

cgc gca ttc ttc cgt gtg cca aaa tgg atg tgg cag gga ttt ctt ggt 1442
 Arg Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly
 465 470 475

tca agt ctt tct tca gca gac ctc atg tta ttt gcc ttc tac atg ttt 1490
 Ser Ser Leu Ser Ser Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe
 480 485 490 495

att att gca cca aat gac atg aga aaa ggc ttg atc aga cat ctt tta 1538
 Ile Ile Ala Pro Asn Asp Met Arg Lys Gly Leu Ile Arg His Leu Leu
 500 505 510

tct gat cct act ggt gca aca ttg ata aga act tat ctt aca ttt 1583
 Ser Asp Pro Thr Gly Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
 515 520 525

tagagtaaac tcctcctaca ataattgttg aatcagaggc ctcattactt cagattcata 1643
 acagaaatcg cggctctctcg aggcattgta tataacattt tcactagctt aata 1697

<210> 46
 <211> 526
 <212> PRT
 <213> *Lycopersicon esculentum*
 <400> 46

Met Glu Cys Val Gly Val Gln Asn Val Gly Ala Met Ala Val Leu Thr
 1 5 10 15

Arg Pro Arg Leu Asn Arg Trp Ser Gly Gly Glu Leu Cys Gln Glu Lys
 20 25 30

Ser Ile Phe Leu Ala Tyr Glu Gln Tyr Glu Ser Lys Cys Asn Ser Ser
 35 40 45

Ser Gly Ser Asp Ser Cys Val Val Asp Lys Glu Asp Phe Ala Asp Glu
 50 55 60

Glu Asp Tyr Ile Lys Ala Gly Gly Ser Gln Leu Val Phe Val Gln Met
 65 70 75 80

Gln	Gln	Lys	Lys	Asp	Met	Asp	Gln	Gln	Ser	Lys	Leu	Ser	Asp	Glu	Leu			
				85					90					95				
Arg	Gln	Ile	Ser	Ala	Gly	Gln	Thr	Val	Leu	Asp	Leu	Val	Val	Ile	Gly			
			100					105					110					
Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	Gly			
		115					120					125						
Leu	Asn	Val	Gly	Leu	Val	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr			
	130					135					140							
Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Gln	Ala	Cys	Ile			
145					150					155					160			
Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Asp	Glu	Pro			
				165					170					175				
Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Phe	Leu	His			
			180					185					190					
Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ala	Gly	Val	Leu	Tyr	Leu	Asn			
		195					200					205						
Ser	Lys	Val	Asp	Arg	Ile	Val	Glu	Ala	Thr	Asn	Gly	Gln	Ser	Leu	Val			
	210					215					220							
Glu	Cys	Glu	Gly	Asp	Val	Val	Ile	Pro	Cys	Arg	Phe	Val	Thr	Val	Ala			
225					230					235					240			
Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu	Gln	Tyr	Glu	Leu	Gly	Ser	Pro			
				245					250					255				
Arg	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Asp	Asn			
			260					265						270				
Asn	Pro	Phe	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr			
		275					280					285						
Leu	Arg	His	Asp	Ala	Gln	Ser	Leu	Glu	Ala	Lys	Tyr	Pro	Thr	Phe	Leu			
	290					295					300							
Tyr	Ala	Met	Pro	Met	Ser	Pro	Thr	Arg	Val	Phe	Phe	Glu	Glu	Thr	Cys			
305					310					315					320			
Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Lys	Leu			
				325					330					335				
Met	Leu	Arg	Leu	Asn	Thr	Leu	Gly	Val	Arg	Ile	Lys	Glu	Ile	Tyr	Glu			
			340					345					350					
Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu			
		355					360					365						
Gln	Lys	Thr	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala			
	370					375					380							
Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Cys	Ala			
385					390					395					400			
Ser	Val	Leu	Ala	Asn	Ile	Leu	Arg	Gln	His	Tyr	Ser	Lys	Asn	Met	Leu			
				405					410					415				
Thr	Ser	Ser	Ser	Ile	Pro	Ser	Ile	Ser	Thr	Gln	Ala	Trp	Asn	Thr	Leu			
				420				425					430					
Trp	Pro	Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu			
		435					440					445						
Ala	Leu	Ile	Leu	Gln	Leu	Asp	Ile	Glu	Gly	Ile	Arg	Ser	Phe	Phe	Arg			
	450					455					460							

Ala	Phe	Phe	Arg	Val	Pro	Lys	Trp	Met	Trp	Gln	Gly	Phe	Leu	Gly	Ser
465					470					475					480
Ser	Leu	Ser	Ser	Ala	Asp	Leu	Met	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Ile
				485					490					495	
Ile	Ala	Pro	Asn	Asp	Met	Arg	Lys	Gly	Leu	Ile	Arg	His	Leu	Leu	Ser
			500					505					510		
Asp	Pro	Thr	Gly	Ala	Thr	Leu	Ile	Arg	Thr	Tyr	Leu	Thr	Phe		
		515					520					525			

<210> 47

<211> 510

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(510)

<223> coding for epsilon-cyclase specific probe

<400> 47

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ggcagcaggc aaagcaaagg ttgtttgttg ttgttgttga gagacactcc aatccaaaca 60
gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120
agaatcatta ctaacaatca atgagtatga gagctggaca catgacggca acaatggcgg 180
cttttacatg cctagggtt atgactagca tcagatacac gaagcaaatt aagtgaacg 240
ctgctaaaag ccagctagtc gttaaacaag agattgagga ggaagaagat tatgtgaaag 300
ccggtggatc ggagctgctt ttgtttcaaa tgcaacagaa taagtccatg gatgcacagt 360
ctagcctatc ccaaaagctc ccaagggtac caataggagg aggaggagac agtaactgta 420
tactggattt ggttgtaatt ggttggtggtc ctgctggcct tgctcttgct ggagaatcag 480
ccaagctagg cttgaatgtc gcacttatcg                               510

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<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 48

ggcagcaggc aaagcaaagg

20

<210> 49

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 49

cgataagtgc gacattcaag c

21

<210> 50

<211> 734

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(734)

<223> fragment of epsilon cyclase gene obtain by iPCR
comprising part of promoter region

<400> 50

```
ctaacaatca atgagtagag agctggacac atgacggcaa caatggcggc ttttacatgc 60
cctaggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc 120
cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cggtgatcg 180
gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc 240
caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat 300
gatattttaga tagattagct atcacctgtg ctgtgggtgtg cagctcccaa gggctttacc 360
gatagtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg 420
tgagaatggt gagaaagagg tttgacaaat cgggtgtttga atgaggttaa atggagttaa 480
attaaaataa agagaagaga aagattaaga ggggtgatggg gatattaag acggscaata 540
tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct 600
tggctgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta 660
ttgaatgcaa agcaaagcaa aggttgtttg ttgttgttgt tgagagacac tccaatccaa 720
acagatacaa ggcg                                     734
```

<210> 51

<211> 280

<212> DNA

<213> *Tagetes erecta*

<220>

<221> misc_feature

<222> (1)..(280)

<223> fragment of epsilon cyclase gene obtain by
TAIL-PCR comprising part of promoter region

<400> 51

```
gtcgagtatg gagttcaatt aaaataaaga gaagaraaag attaagaggg tgatggggat 60
attaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaac acatacaacg 120
tggctttaa agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc 180
aaattcaatt caattctatt gaatgcaaag caaagcaaag caaaggttgt ttgttgttgt 240
tgttgagaga cactccaatc caaacagata caaggcgtga 280
```

<210> 52

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 52

```
cgccttgat ctgtttggat tgg                                     23
```

<210> 53

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 53

```
ctaacaatca atgagtatga gagc                                     24
```

<210> 54

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 54

agagcaaggc cagcaggacc acaacc

26

<210> 55

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 55

ccttgggagc ttttgggata ggctag

26

<210> 56

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 56

tcacgccttg tatctgttg gattgg

26

<210> 57

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 57

gtcgagtatg gagtt

15

<210> 58

<211> 734

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(734)

<223> coding for epsilon-cyclase genomic iPCR-fragment

<400> 58

ctaacaatca	atgagtagag	agctggacac	atgacggcaa	caatggcggc	ttttacatgc	60
cctaggttta	tgactagcat	cagatacacg	aagcaaatta	agtgcaacgc	tgctaaaagc	120
cagctagtcg	ttaaacaaga	gattgaggag	gaagaagatt	atgtgaaagc	cggtaggatcg	180
gagctgcttt	ttgttcaaat	gcaacagaat	aagtccatgg	atgcacagtc	tagcctatcc	240
caaaaggcca	ctccagactt	aattgcttat	aaataaataa	atatgttttt	taggaataat	300
gatatttaga	tagattagct	atcacctgtg	ctgtgggtgtg	cagctcccaa	gggtcttacc	360
gatatgaaaa	tcgttagtta	tgattaatac	ttgggagggtg	ggggattata	ggctttgttg	420
tgagaatggt	gagaaagagg	tttgacaaat	cgggtgtttga	atgaggttta	atggagttta	480
attaaaataa	agagaagaga	aagattaaga	gggtgatggg	gatattaaag	acggscaata	540
tagtgatgcc	acgtagaaaa	aggtaagtga	aaacatacaa	cgtggcttta	aaagatggct	600
tggctgctaa	tcaactcaac	tcaactcata	tcctatccat	tcaaattcaa	ttcaattcta	660

ttgaatgcaa agcaaagcaa aggttgtttg ttgttgttgt tgagagacac tccaatccaa 720
acagatacaa ggcg 734

<210> 59

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 59

ctcgagagta aaatcgttag ttatg 25

<210> 60

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 60

ccatggccat tgattgtag taatgattc 29

<210> 61

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 61

ccatggtaat ttgcttcgtg tatctgatg 29

<210> 62

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 62

ccatggcgct agcagcgaca gtaatg 26

<210> 63

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 63

gatatccggt gtgagggaac tag 23

<210> 64

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 64

gcaagctcga cagctacaaa cc

22

<210> 65

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 65

gaagcatgca gctagcagcg acag

24

<210> 66

<211> 1795

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: coding for
ketolase - 35S terminator construct

<400> 66

```

ccatggcgct agcagcgaca gtaatgttgg agcagcttac cggaagcgct gaggcactca 60
aggagaagga gaaggaggtt gcaggcagct ctgacgtgtt gcgtacatgg gcgacccagt 120
actcgcttcc gtcagaggag tcagacgcgg cccgcccggg actgaagaat gcctacaagc 180
caccaccttc cgacacaaaag ggcatacaca tggcgctagc tgtcatcggc tcctggggccg 240
cagtgttcct ccacgccatt tttcaaatca agcttccgac ctcccttgac cagctgcact 300
ggctgcccgt gtcagatgcc acagctcagc tggttagcgg cagcagcagc ctgctgcaca 360
tcgtcgtagt attctttgtc ctggagttcc tgtacacagg cctttttatc accacgcatg 420
atgctatgca tggcaccatc gccatgagaa acaggcagct taatgacttc ttgggcagag 480
tatgcatctc cttgtacgcc tggtttgatt acaacatgct gcaccgcaag cattggggagc 540
accacaacca cactggcgag gtgggcaagg accctgactt ccacagggga aaccctggca 600
ttgtgccctg gtttgccagc ttcattgtcca gctacatgtc gatgtggcag tttgcgcgcc 660
tcgcatggtg gacggtggtc atgcagctgc tgggtgcgcc aatggcgaac ctgctggtgt 720
tcatggcggc cgcgcccatt ctgtccgcct tccgcttgtt ctactttggc acgtacatgc 780
cccacaagcc tgagcctggc gccgcgtcag gctcttcacc agccgtcatg aactgggtgga 840
agtcgcgcac tagccaggcg tccgacctgg tcagctttct gacctgtac cacttcgacc 900
tgcactggga gcaccaccgc tggccctttg ccccttggtg ggagctgcc aactgccgcc 960
gcctgtcttg ccgaggtctg gttcctgcct agctggacac actgcagtgg gccctgctgc 1020
cagctgggca tgcctgcagg tcgacggatc cccgggaatt cggtagctg aaatcaccag 1080
tctctctcta caaatctatc tctctctatt ttctccataa ataatgtgtg agtagtttcc 1140
cgataaggga aattagggtt cttatagggt ttcgtcatg tgttgagcat ataagaaacc 1200
cttagtatgt atttgtattt gtaaaatact tctatcaata aaatttctaa ttcctaaaac 1260
caaaatccag tactaaaatc cagatctcct aaagtcccta tagatctttg tcgtgaatat 1320
aaaccagaca cgagacgact aaacctggag cccagacgcc gttcgaagct agaagtaccg 1380
cttaggcagg aggccgttag ggaaaagatg ctaaggcagg gttgggttac ttgactcccc 1440
cgtaggtttg gtttaaatat gatgaagtgg acggaaggaa ggaggaagac aaggaaggat 1500
aaggttgcag gccctgtgca aggttaagaag atggaaattt gatagaggta cgctactata 1560
cttatactat acgctaaggg aatgcttgta tttataaccct atacccccta ataaccctt 1620
atcaatttaa gaaataatcc gcataagccc ccgcttaaaa attggtatca gagccatgaa 1680
taggtctatg accaaaactc aagaggataa aacctcacca aaatacgaaa gagttcttaa 1740
ctctaaagat aaaagatctt tcaagatcaa aactagttcc ctcacaccgg atatc 1795

```

<210> 67

<211> 28

```

<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
        oligonucleotide primer
<400> 67
gagctcactc actgatttcc attgcttg                28
<210> 68
<211> 37
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
        oligonucleotide primer
<400> 68
cgccgttaag tcgatgtccg ttgatttaaa cagtgtc        37
<210> 69
<211> 34
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
        oligonucleotide primer
<400> 69
atcaacggac atcgacttaa cggcgtttgt aaac          34
<210> 70
<211> 25
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
        oligonucleotide primer
<400> 70
taagctttttt gttgaagaga tttgg                    25
<210> 71
<211> 28
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
        oligonucleotide primer
<400> 71
gtcgactacg taagtttctg cttctacc                  28
<210> 72
<211> 26
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
        oligonucleotide primer

```


<400> 72
 ggatccggtg atacctgcac atcaac 26
 <210> 73
 <211> 28
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer
 <400> 73
 aagcttaccg atagtaaaat cgtaggtt 28
 <210> 74
 <211> 31
 <212> DNA
 <213> Artifical sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer
 <400> 74
 ctcgagctta ccgatagtaa aatcgtagt t 31
 <210> 75
 <211> 28
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer
 <400> 75
 gtcgacaaca acaacaaaca acctttgc 28
 <210> 76
 <211> 28
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer
 <400> 76
 ggatccaaca acaacaaaca acctttgc 28
 <210> 77
 <211> 777
 <212> DNA
 <213> Arabidopsis thaliana
 <220>
 <221> promoter
 <222> (1)..(777)
 <223> modified version of the AP3 promoter
 <400> 77
 gagctcactc actgatttcc attgcttgaa aattgatgat gaactaagat caatccatgt 60
 tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactggtcga 120
 agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagttagga 180
 ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaacccta 240

```

ggggtaatat tctattttcc aaggatcttt agttaaaggg aaatccggga aattattgta 300
atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360
tatatatctc tttcttctta tttcccaa ataacagacaa aagtagaata ttggctttta 420
acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgc 480
aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540
ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600
tcacttagtt ttcactcaact tctgaactta cctttcatgg attaggcaat actttccatt 660
tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720
tctttcttct cattatatct cttgtcctct ccaccaaata tcttcaacaa aaagctt 777

```

<210> 78

<211> 212

<212> DNA

<213> Solanum tuberosum

<220>

<221> intron

<222> (1)..(212)

<223> PIV2 intron of ST-LS1 gene

<400> 78

```

gtcgactacg taagtttctg cttctacctt tgatatatat ataataatta tcattaatta 60
gtagtaatat aatatttcaa atattttttt caaaataaaa gaatgtagta tatagcaatt 120
gcttttctgt agtttataag tgtgtatatt ttaatttata acttttctaa tatatgacca 180
aaatttggtg atgtgcaggt atcaccggat cc 212

```

<210> 79

<211> 358

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(358)

<223> coding for sense-strand of epsilon cyclase
promoter directed dsRNA

<400> 79

```

aagcttaccg atagtaaaat cgtagttat gattaatact tgggaggtgg gggattatag 60
gctttgttgt gagaatggtg agaaagaggt ttgacaaatc ggtggttgaa tgaggttaaa 120
tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180
cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240
aagatggctt ggctgcta atcaactca cactcatat cctatccatt caaattcaat 300
tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtt tttgttggtt ttgtcgac 358

```

<210> 80

<211> 361

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(361)

<223> coding for antisense-strand of epsilon cyclase
promoter directed dsRNA

<400> 80

```

ctcgagctta ccgatatgaa aatcgttagt tatgattaat acttgggagg tgggggatta 60
taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgaggtt 120
aatggaggtt taattaaaaa aaagagaaga gaaagattaa gagggatgat gggatattaa 180
agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240
taaaagatgg cttggctgct aatcaactca actcaactca tatcctatcc attcaaattc 300
aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttggtt ttgttgatc 360
c 361

```

<210> 81
 <211> 1537
 <212> DNA
 <213> Cucumis sativus
 <220>
 <221> promoter
 <222> (1)..(1537)
 <223> promoter of chromoplast-specific
 carotenoid-associated protein (CHRC)

<400> 81
 gagctctaca aattaggggtt actttattca ttttcatcca ttctctttat tgttaaattt 60
 tgtacattta ttcaataata ttatatgttt attacaaatt ctacttttct tattcatacc 120
 tattcactca agcctttacc atcttccttt tctatttcaa tactatttct acttcatttt 180
 tcacgttttt aacatctttc tttatttctt gtccacttcg tttagggatg cctaattgtcc 240
 caaattttcat ctctcgtagt aacacaaaac caatgtaatg ctacttctct ctacattttt 300
 aatacaataa aagtgaacaa aaatatctat aaataaacia atatataat tttgttagac 360
 gctgtctcaa cccatcaatt aaaaaatttt gttatatttc tactttacct actaaatttg 420
 tttctcatat ttacctttta acccccacaa aaaaaaatta taaaaaagaa agaaaaaagc 480
 taaaccctat ttaaatagct aactataaga tcttaaaatt atcctcatca gtgtatagtt 540
 taattgggta ttaacttata acattatata tctatgacat atactctctc ctacttattt 600
 ctcacatttt ttaacttaag aaaatagtca taacatagtc taaaattcaa acatccacat 660
 gctctaattt gattaacaaa aagttagaaa tattttattta aataaaaaaag actaataaat 720
 atataaaatg aatgttcata cgcagacca tttagagatg agtatgcttt cacatgctga 780
 gattattttc aaaactaagg ttgttagcaat attaaatcaa taaaattatt ataaataaca 840
 aaattaacct gctcgtgttt gctgtatatg ggaggctaca aaataaatta aactaaagat 900
 gattatgttt tagacatttt ttctatctgt attagtttat acatattaat tcaggagctg 960
 cacaacccaa ttctattttc gttccttggt ggctgggttt ctcacaaggt tcaatagtca 1020
 atattagggt ttattggact tttaatagta tcaaacaaat ctatgtgtga acttaaaaat 1080
 tgtattaaat atttagggta acctgttgcc gtttttagaa taatgtttct tcttaataca 1140
 cgaaagcgta ttgtgtattc attcatttgg cgcctcacat gcttcggttg gctcgttta 1200
 gtctctgcct tctttgtata ttgtactccc cctcttcccta tgccacgtgt tctgagctta 1260
 acaagccacg ttgcgtgcc a ttgccaaaca agtcatttta acttcacaag gtccgatttg 1320
 acctccaaaa caacgacaag tttccgaaca gtcgcgaaga tcaagggtat aatcgtcttt 1380
 ttgaattcta tttctcttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt 1440
 taaaacgtag ctgctgttta agtaaattccc agtccttcag tttgtgcttt tgtgtgtttt 1500
 gtttctctga tttacggaat ttggaaataa taagctt 1537

<210> 82
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 82
 gagctctaca aattaggggtt ac 22

<210> 83
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 83
 aagcttatta tttccaaatt ccg 23